



#4

## SEQUENCE LISTING

<110> Vernet, Corine A. M.  
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Rastelli, Luca  
Herrman, John L

<120> Novel Proteins and Nucleic Acids Encoding Same

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<140> 09/825,751

<141> 2001-04-03

<150> 60/194,314

<151> 2000-04-03

<150> 60/225,693

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<170> PatentIn Ver. 2.1

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Tyr Arg Ala Gly Ala Cys Phe Ser Val Leu Phe Gly Gly Arg Cys Ala	
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ggt cac cgc tgc ctg tgc tat gat ggc ttc atg gcc acg cca gac atg	2927
Gly His Arg Cys Leu Cys Tyr Asp Gly Phe Met Ala Thr Pro Asp Met	
960 965 970 975	
agg aca tgt gtt gat gtg gat gag tgt gac ctg aac cct cac atc tgc	2975
Arg Thr Cys Val Asp Val Asp Glu Cys Asp Leu Asn Pro His Ile Cys	
980 985 990	
ctc cat ggg gac tgc gag aac acg aag ggt tcc ttt gtc tgc cac tgt	3023
Leu His Gly Asp Cys Glu Asn Thr Lys Gly Ser Phe Val Cys His Cys	
995 1000 1005	
cag ctg ggc tac atg gtc agg aag ggg gcc aca ggc tgc tct gat gtg	3071
Gln Leu Gly Tyr Met Val Arg Lys Gly Ala Thr Gly Cys Ser Asp Val	
1010 1015 1020	

gat gaa tgc gag gtt gga gga cac aac tgt gac agt cac gcc tcc tgt 3119  
Asp Glu Cys Glu Val Gly Gly His Asn Cys Asp Ser His Ala Ser Cys  
1025 1030 1035  
ctc aac atc ccg ggg agt ttc agc tgt agg tgc ctg cca ggc tgg gtg 3167  
Leu Asn Ile Pro Gly Ser Phe Ser Cys Arg Cys Leu Pro Gly Trp Val  
1040 1045 1050 1055  
ggg gat ggc ttc gaa tgt cac gac ctg gat gaa tgc gtc tcc cag gag 3215  
Gly Asp Gly Phe Glu Cys His Asp Leu Asp Glu Cys Val Ser Gln Glu  
1060 1065 1070  
cac cgg tgc agc cca aga ggt gac tgt ctc aat gtc cct ggc tcc tac 3263  
His Arg Cys Ser Pro Arg Gly Asp Cys Leu Asn Val Pro Gly Ser Tyr  
1075 1080 1085  
cgc tgc acc tgc cgc cag ggc ttt gcc ggg gat ggc ttc ttc tgc gaa 3311  
Arg Cys Thr Cys Arg Gln Gly Phe Ala Gly Asp Gly Phe Phe Cys Glu  
1090 1095 1100  
gac agg gat gaa tgt gcc gag aac gtg gac ctc tgt gac aac ggg 3356  
Asp Arg Asp Glu Cys Ala Glu Asn Val Asp Leu Cys Asp Asn Gly  
1105 1110 1115  
tagtgccctca atgcgccc 3374

<210> 6  
<211> 1118  
<212> PRT  
<213> Homo sapiens

<400> 6  
Gln Gly Gly Ser Cys Val Asn Met Val Gly Ser Phe His Cys Arg Cys  
1 5 10 15  
Pro Val Gly His Arg Leu Ser Asp Ser Ser Ala Ala Cys Glu Asp Tyr  
20 25 30  
Arg Ala Gly Ala Cys Phe Ser Val Leu Phe Gly Gly Arg Cys Ala Gly  
35 40 45  
Asp Leu Ala Gly His Tyr Thr Arg Arg Gln Cys Cys Cys Asp Arg Gly  
50 55 60  
Arg Cys Trp Ala Ala Gly Pro Val Pro Glu Leu Cys Pro Pro Arg Gly  
65 70 75 80

Ser Asn Glu Phe Gln Gln Leu Cys Ala Gln Arg Leu Pro Leu Leu Pro  
 85 90 95

Gly His Pro Gly Leu Phe Pro Gly Leu Leu Gly Phe Gly Ser Asn Gly  
 100 105 110

Met Gly Pro Pro Leu Gly Pro Ala Arg Leu Asn Pro His Gly Ser Asp  
 115 120 125

Ala Arg Gly Ile Pro Ser Leu Gly Pro Gly Asn Ser Asn Ile Gly Thr  
 130 135 140

Ala Thr Leu Asn Gln Thr Ile Asp Ile Cys Arg His Phe Thr Asn Leu  
 145 150 155 160

Cys Leu Asn Gly Arg Cys Leu Pro Thr Pro Ser Ser Tyr Arg Cys Glu  
 165 170 175

Cys Asn Val Gly Tyr Thr Gln Asp Val Arg Gly Glu Cys Ile Asp Val  
 180 185 190

Asp Glu Cys Thr Ser Ser Pro Cys His His Gly Asp Cys Val Asn Ile  
 195 200 205

Pro Gly Thr Tyr His Cys Arg Cys Tyr Pro Gly Phe Gln Ala Thr Pro  
 210 215 220

Thr Arg Gln Ala Cys Val Asp Val Asp Glu Cys Ile Val Ser Gly Gly  
 225 230 235 240

Leu Cys His Leu Gly Arg Cys Val Asn Thr Glu Gly Ser Phe Gln Cys  
 245 250 255

Val Cys Asn Ala Gly Phe Glu Leu Ser Pro Asp Gly Lys Asn Cys Val  
 260 265 270

Asp His Asn Glu Cys Ala Thr Ser Thr Met Cys Val Asn Gly Val Cys  
 275 280 285

Leu Asn Glu Asp Gly Ser Phe Ser Cys Leu Cys Lys Pro Gly Phe Leu  
 290 295 300

Leu Ala Pro Gly Gly His Tyr Cys Met Asp Ile Asp Glu Cys Gln Thr  
 305 310 315 320

Pro Gly Ile Cys Val Asn Gly His Cys Thr Asn Thr Glu Gly Ser Phe  
 325 330 335

Arg Cys Gln Cys Leu Gly Gly Leu Ala Val Gly Thr Asp Gly Arg Val  
 340 345 350

Cys Val Asp Thr His Val Arg Ser Thr Cys Tyr Gly Ala Ile Glu Lys  
 355 360 365

Gly Ser Cys Ala Arg Pro Phe Pro Gly Thr Val Thr Lys Ser Glu Cys  
 370 375 380

Cys Cys Ala Asn Pro Asp His Gly Phe Gly Glu Pro Cys Gln Leu Cys  
 385 390 395 400

Pro Ala Lys Asn Ser Ala Glu Phe Gln Ala Leu Cys Ser Ser Gly Leu  
 405 410 415

Gly Ile Thr Thr Asp Gly Arg Asp Ile Asn Glu Cys Ala Leu Asp Pro  
 420 425 430

Glu Val Cys Ala Asn Gly Val Cys Glu Asn Leu Arg Gly Ser Tyr Arg  
 435 440 445

Cys Val Cys Asn Leu Gly Tyr Glu Ala Gly Ala Ser Gly Lys Asp Cys  
 450 455 460

Thr Asp Val Asp Glu Cys Ala Leu Asn Ser Leu Leu Cys Asp Asn Gly  
 465 470 475 480

Trp Cys Gln Asn Ser Pro Gly Ser Tyr Ser Cys Ser Cys Pro Pro Gly  
 485 490 495

Phe His Phe Trp Gln Asp Thr Glu Ile Cys Lys Asp Val Asp Glu Cys  
 500 505 510

Leu Ser Ser Pro Cys Val Ser Gly Val Cys Arg Asn Leu Ala Gly Ser  
 515 520 525

Tyr Thr Cys Lys Cys Gly Pro Gly Ser Arg Leu Asp Pro Ser Gly Thr  
 530 535 540

Phe Cys Leu Asp Ser Thr Lys Gly Thr Cys Trp Leu Lys Ile Gln Glu  
 545 550 555 560

Ser Arg Cys Glu Val Asn Leu Gln Gly Ala Ser Leu Arg Ser Glu Cys  
 565 570 575

Cys Ala Thr Leu Gly Ala Ala Trp Gly Ser Pro Cys Glu Arg Cys Glu  
 580 585 590



Ile Asp Pro Ala Cys Ala Arg Gly Phe Ala Arg Met Thr Gly Val Thr  
 595 600 605

Cys Asp Asp Val Asn Glu Cys Glu Ser Phe Pro Gly Val Cys Pro Asn  
 610 615 620

Gly Arg Cys Val Asn Thr Ala Gly Ser Phe Arg Cys Glu Cys Pro Glu  
 625 630 635 640

Gly Leu Met Leu Asp Ala Ser Gly Arg Leu Cys Val Asp Val Arg Leu  
 645 650 655

Glu Pro Cys Phe Leu Arg Trp Asp Glu Asp Glu Cys Gly Val Thr Leu  
 660 665 670

Pro Gly Lys Tyr Arg Met Asp Val Cys Cys Cys Ser Ile Gly Ala Val  
 675 680 685

Trp Gly Val Glu Cys Glu Ala Cys Pro Asp Pro Glu Ser Leu Glu Phe  
 690 695 700

Ala Ser Leu Cys Pro Arg Gly Leu Gly Phe Ala Ser Arg Asp Phe Leu  
 705 710 715 720

Ser Gly Arg Pro Phe Tyr Lys Asp Val Asn Glu Cys Lys Val Phe Pro  
 725 730 735

Gly Leu Cys Thr His Gly Thr Cys Arg Asn Thr Val Gly Ser Phe His  
 740 745 750

Cys Ala Cys Ala Gly Gly Phe Ala Leu Asp Ala Gln Glu Arg Asn Cys  
 755 760 765

Thr Asp Ile Asp Glu Cys Arg Ile Ser Pro Asp Leu Cys Gly Gln Gly  
 770 775 780

Thr Cys Val Asn Thr Pro Gly Ser Phe Glu Cys Glu Cys Phe Pro Gly  
 785 790 795 800

Tyr Glu Ser Gly Phe Met Leu Met Lys Asn Cys Met Asp Val Asp Glu  
 805 810 815

Cys Ala Arg Asp Pro Leu Leu Cys Arg Gly Gly Thr Cys Thr Asn Thr  
 820 825 830

Asp Gly Ser Tyr Lys Cys Gln Cys Pro Pro Gly His Glu Leu Thr Ala  
 835 840 845

Lys Gly Thr Ala Cys Glu Asp Ile Asp Glu Cys Ser Leu Ser Asp Gly  
 850 855 860

Leu Cys Pro His Gly Gln Cys Val Asn Val Ile Gly Ala Phe Gln Cys  
 865 870 875 880

Ser Cys His Ala Gly Phe Gln Ser Thr Pro Asp Arg Gln Gly Cys Val  
 885 890 895

Asp Ile Asn Glu Cys Arg Val Gln Asn Gly Gly Cys Asp Val His Arg  
 900 905 910

Ile Asn Thr Glu Gly Ser Tyr Arg Cys Ser Cys Gly Gln Gly Tyr Ser  
 915 920 925

Leu Met Pro Asp Gly Arg Ala Cys Ala Asp Val Asp Glu Cys Glu Glu  
 930 935 940

Asn Pro Arg Val Cys Asp Gln Gly His Cys Thr Asn Met Pro Gly Gly  
 945 950 955 960

His Arg Cys Leu Cys Tyr Asp Gly Phe Met Ala Thr Pro Asp Met Arg  
 965 970 975

Thr Cys Val Asp Val Asp Glu Cys Asp Leu Asn Pro His Ile Cys Leu  
 980 985 990

His Gly Asp Cys Glu Asn Thr Lys Gly Ser Phe Val Cys His Cys Gln  
 995 1000 1005

Leu Gly Tyr Met Val Arg Lys Gly Ala Thr Gly Cys Ser Asp Val Asp  
 1010 1015 1020

Glu Cys Glu Val Gly Gly His Asn Cys Asp Ser His Ala Ser Cys Leu  
 1025 1030 1035 1040

Asn Ile Pro Gly Ser Phe Ser Cys Arg Cys Leu Pro Gly Trp Val Gly  
 1045 1050 1055

Asp Gly Phe Glu Cys His Asp Leu Asp Glu Cys Val Ser Gln Glu His  
 1060 1065 1070

Arg Cys Ser Pro Arg Gly Asp Cys Leu Asn Val Pro Gly Ser Tyr Arg  
 1075 1080 1085

Cys Thr Cys Arg Gln Gly Phe Ala Gly Asp Gly Phe Phe Cys Glu Asp  
 1090 1095 1100

Arg Asp Glu Cys Ala Glu Asn Val Asp Leu Cys Asp Asn Gly  
 1105 1110 1115

<210> 7  
 <211> 439  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (2)..(292)

<400> 7  
 t cac ggg aat aag cct ggg ccc gtc cct ttg att tcc aac aag atc tgc 49  
 His Gly Asn Lys Pro Gly Pro Val Pro Leu Ile Ser Asn Lys Ile Cys  
 1 5 10 15  
 aac cac agg gac gtg tac ggt ggc atc atc tcc ccc tcc atg ctc tgc 97  
 Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu Cys  
 20 25 30  
 gcg ggc tac ctg acg ggt ggc gtg gac agc tgc cag ggg gac agc ggg 145  
 Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly  
 35 40 45  
 ggg ccc ctg gtg tgt caa gag agg agg ctg tgg aag tta gtg gga gcg 193  
 Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala  
 50 55 60  
 acc agc ttt ggc atc ggc tgc gca gag gtg aac aag cct ggg gtg tac 241  
 Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr  
 65 70 75 80  
 acc gtg tca cct cct tcc tgg act gga tcc acg agc aga tgg aga gag 289  
 Thr Val Ser Pro Pro Ser Trp Thr Gly Ser Thr Ser Arg Trp Arg Glu  
 85 90 95  
 acc taaaaacctg aagaggaagg ggataagtag ccacctgagt tcctgaggtg 342  
 Thr  
 atgaagacag cccgatcctc ccctggactc ccgtgtagga acctgcacac gagcagacac 402  
 ccttgagact ctgagttccg gcaccagtag caggccc 439

<210> 8

<211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 His Gly Asn Lys Pro Gly Pro Val Pro Leu Ile Ser Asn Lys Ile Cys  
           1                  5                  10                  15  
 Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu Cys  
                   20                  25                  30  
 Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly  
           35                  40                  45  
 Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala  
           50                  55                  60  
 Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr  
           65                  70                  75                  80  
 Thr Val Ser Pro Pro Ser Trp Thr Gly Ser Thr Ser Arg Trp Arg Glu  
                   85                  90                  95  
 Thr

<210> 9  
 <211> 410  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (3)..(410)

<400> 9  
 tg tca ttg tcc ttt tac cta tta tat ttt ttc ata ctc tgt gaa aac       47  
   Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn  
           1                  5                  10                  15  
 aaa tca gtt gcc gga cta acc atg acc tat gat gga aat aat cca gtg       95  
 Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val  
                   20                  25                  30  
 aca tct cat aga gat gtg cca ctt tct tat tgc aac tca gac tgc aat       143  
 Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn

35	40	45	
tgt gat gaa agt cag tgg gaa cca gtc	tgt ggg aac aat gga ata act	191	
Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr			
50	55	60	
tac ctg tca cct tgt cta gca gga tgc aaa tcc tca agt ggt att aaa	239		
Tyr Leu Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Ile Lys			
65	70	75	
aag cat aca gtg ttt tat aac tgt agt tgt gtg gaa gta act ggt ctc	287		
Lys His Thr Val Phe Tyr Asn Cys Ser Cys Val Glu Val Thr Gly Leu			
80	85	90	95
cag aac aga aat tac tca gcg cac ttg ggt gaa tgc cca aga gat aat	335		
Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asn			
100	105	110	
act tgt aca agg aaa ttt ttc atc tat gtt gca att caa gtc ata aac	383		
Thr Cys Thr Arg Lys Phe Phe Ile Tyr Val Ala Ile Gln Val Ile Asn			
115	120	125	
tct ttg ttc tct gca aca gga ggt acc	410		
Ser Leu Phe Ser Ala Thr Gly Gly Thr			
130	135		
<210> 10			
<211> 136			
<212> PRT			
<213> Homo sapiens			
<400> 10			
Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn Lys			
1	5	10	15
Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val Thr			
20	25	30	
Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn Cys			
35	40	45	
Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr Tyr			
50	55	60	
Leu Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Ile Lys Lys			
65	70	75	80

His Thr Val Phe Tyr Asn Cys Ser Cys Val Glu Val Thr Gly Leu Gln  
85 90 95

Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asn Thr  
100 105 110

Cys Thr Arg Lys Phe Phe Ile Tyr Val Ala Ile Gln Val Ile Asn Ser  
115 120 125

Leu Phe Ser Ala Thr Gly Gly Thr  
130 135

<210> 11  
<211> 322  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (3)..(320)

<400> 11  
tg gca gcc ctg gag gag ccg atg gtg gac ctg gac ggc gag ctg cct 47  
Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro  
1 5 10 15  
ttc gtg cgg ccc ctg ccc cac att gcc gtg ctc cag gac gag ctg ccg 95  
Phe Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro  
20 25 30  
caa ctc ttc cag gat gac gac gtc ggg gcc gat gag gaa gag gca gag 143  
Gln Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Glu Ala Glu  
35 40 45  
ttg cgg ggc gaa cac acg ctc aca gag aag ttt gtc tgc ctg gat gac 191  
Leu Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp  
50 55 60  
tcc ttt ggc cat gac tgc agc ttg acc tgt gat gac tgc agg aac gga 239  
Ser Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly  
65 70 75  
ggg acc tgc ctc ctg ggc ctg gat ggc tgt gat tgc ccc gag ggg tgg 287  
Gly Thr Cys Leu Leu Gly Leu Asp Gly Cys Asp Cys Pro Glu Gly Trp  
80 85 90 95

act ggg gtt att tgc aat gag att tgt cct ccg ga 322  
 Thr Gly Val Ile Cys Asn Glu Ile Cys Pro Pro  
 100 105

<210> 12  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro Phe  
 1 5 10 15  
 Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro Gln  
 20 25 30  
 Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Glu Ala Glu Leu  
 35 40 45  
 Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp Ser  
 50 55 60  
 Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly Gly  
 65 70 75 80  
 Thr Cys Leu Leu Gly Leu Asp Gly Cys Asp Cys Pro Glu Gly Trp Thr  
 85 90 95  
 Gly Val Ile Cys Asn Glu Ile Cys Pro Pro  
 100 105

<210> 13  
 <211> 1332  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (2)..(1306)

<400> 13  
 c gcc ttc atg ctg ccg gcg ggc tgc tcg cgc cgg ctg gtg gcc gag ctg 49  
 Ala Phe Met Leu Pro Ala Gly Cys Ser Arg Arg Leu Val Ala Glu Leu  
 1 5 10 15

cag ggc gcc ctg gac gcc tgc gca cag cga caa ttg caa ttg gag cag	97
Gln Gly Ala Leu Asp Ala Cys Ala Gln Arg Gln Leu Gln Leu Glu Gln	
20 25 30	
agc ctg cgc gtt tgc cgt cgg ctg ctg cat gcc tgg gaa cca act ggg	145
Ser Leu Arg Val Cys Arg Arg Leu Leu His Ala Trp Glu Pro Thr Gly	
35 40 45	
acc cgg gct ttg aag cca cct cca ggg cca gaa act aat gga gag gac	193
Thr Arg Ala Leu Lys Pro Pro Pro Gly Pro Glu Thr Asn Gly Glu Asp	
50 55 60	
ccc ctt cca gca tgc aca ccc agt cca caa gac ctc aaa gag ttg gag	241
Pro Leu Pro Ala Cys Thr Pro Ser Pro Gln Asp Leu Lys Glu Leu Glu	
65 70 75 80	
ttt ctg acc cag gca ctg gag aag gct gta cga gtt cga aga ggc atc	289
Phe Leu Thr Gln Ala Leu Glu Lys Ala Val Arg Val Arg Arg Gly Ile	
85 90 95	
act aag gcc gaa gag aga gac aag gcc ccc agc ctg aaa tct agg tcc	337
Thr Lys Ala Glu Glu Arg Asp Lys Ala Pro Ser Leu Lys Ser Arg Ser	
100 105 110	
att gtc acc tct tct ggc acg aca gcc tcc gcc cca ccg cat tcc cca	385
Ile Val Thr Ser Ser Gly Thr Thr Ala Ser Ala Pro Pro His Ser Pro	
115 120 125	
ggc caa gct ggt ggc cat gct tca gac acg aga ccc acc aag ggc ctc	433
Gly Gln Ala Gly Gly His Ala Ser Asp Thr Arg Pro Thr Lys Gly Leu	
130 135 140	
cgc cag acc acg gtg cct gcc aag ggc cac cct gag cgc cgg ctg ctg	481
Arg Gln Thr Thr Val Pro Ala Lys Gly His Pro Glu Arg Arg Leu Leu	
145 150 155 160	
tca gtg ggg gat ggg acc cgt gtt ggg atg gga gcc cga acc ccc agg	529
Ser Val Gly Asp Gly Thr Arg Val Gly Met Gly Ala Arg Thr Pro Arg	
165 170 175	
cct ggg gcg ggc ctc agg gac cag caa atg gcc cca tcc gct gct cct	577
Pro Gly Ala Gly Leu Arg Asp Gln Gln Met Ala Pro Ser Ala Ala Pro	
180 185 190	
cag gcc cca gaa gcc ttc aca ctc aag gag aag ggg cac ctg ctg cgg	625
Gln Ala Pro Glu Ala Phe Thr Leu Lys Glu Lys Gly His Leu Leu Arg	
195 200 205	



ctg cct gcg gca ttc agg aaa gca gct tcc cag aac tcg agc ctg tgg	673
Leu Pro Ala Ala Phe Arg Lys Ala Ala Ser Gln Asn Ser Ser Leu Trp	
210 215 220	
gcc cag ctc agt tcc aca cag acc agt gat tcc acg gat gcc gcc gct	721
Ala Gln Leu Ser Ser Thr Gln Thr Ser Asp Ser Thr Asp Ala Ala Ala	
225 230 235 240	
gcc aaa acc cag ttc ctc cag aac atg cag aca gct tca ggc ggg ccc	769
Ala Lys Thr Gln Phe Leu Gln Asn Met Gln Thr Ala Ser Gly Gly Pro	
245 250 255	
cag ccc agg ctc agt gct gtg gag gtg gag gcg gag gcg ggg cgc ctg	817
Gln Pro Arg Leu Ser Ala Val Glu Val Glu Ala Glu Ala Gly Arg Leu	
260 265 270	
cgg aag gcc tgc tcg ctg ctg aga ctg cgc atg agg gag gag ctc tca	865
Arg Lys Ala Cys Ser Leu Leu Arg Leu Arg Met Arg Glu Glu Leu Ser	
275 280 285	
gca gcc ccc atg gac tgg atg cag gag tac cgc tgc ctg ctc acg ctg	913
Ala Ala Pro Met Asp Trp Met Gln Glu Tyr Arg Cys Leu Leu Thr Leu	
290 295 300	
gag ggg ctg cag gcc atg gtg ggc cag tgt ctg cac agg ctg cag gag	961
Glu Gly Leu Gln Ala Met Val Gly Gln Cys Leu His Arg Leu Gln Glu	
305 310 315 320	
ctg cgt gca gcg gtg gcg gaa cag cca cca aga cca tgt cct gtg ggg	1009
Leu Arg Ala Ala Val Ala Glu Gln Pro Pro Arg Pro Cys Pro Val Gly	
325 330 335	
agg ccc ccc gga gcc tcg ccg tcc tgt ggg ggt aga gcg gag cct gca	1057
Arg Pro Pro Gly Ala Ser Pro Ser Cys Gly Gly Arg Ala Glu Pro Ala	
340 345 350	
tgg agc ccc cag ctg ctt gtc tac tcc agc acc cag gag ctg cag acc	1105
Trp Ser Pro Gln Leu Leu Val Tyr Ser Ser Thr Gln Glu Leu Gln Thr	
355 360 365	
ctg gcg gcc ctc aag ctg cga gtg gct gtg ctg gac cag cag atc cac	1153
Leu Ala Ala Leu Lys Leu Arg Val Ala Val Leu Asp Gln Gln Ile His	
370 375 380	
ttg gaa aag gtc ctg atg gct gaa ctc ctc ccc ctg gta agc gct gca	1201
Leu Glu Lys Val Leu Met Ala Glu Leu Leu Pro Leu Val Ser Ala Ala	
385 390 395 400	

cag ccg cag ggg ccg ccc tgg ctg gcc ctg tgc cgg gct gtg cac agc 1249  
 Gln Pro Gln Gly Pro Pro Trp Leu Ala Leu Cys Arg Ala Val His Ser  
                     405                    410                    415

ctg ctc tgc gag gga gga gca cgt gtc ctt acc atc ctg cgg gat gaa 1297  
 Leu Leu Cys Glu Gly Gly Ala Arg Val Leu Thr Ile Leu Arg Asp Glu  
                     420                    425                    430

cct gca gtc tgagcctttc ccatgctgcc ctcggc 1332  
 Pro Ala Val  
                     435

<210> 14  
 <211> 435  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
 Ala Phe Met Leu Pro Ala Gly Cys Ser Arg Arg Leu Val Ala Glu Leu  
   1                    5                    10                    15

Gln Gly Ala Leu Asp Ala Cys Ala Gln Arg Gln Leu Gln Leu Glu Gln  
                     20                    25                    30

Ser Leu Arg Val Cys Arg Arg Leu Leu His Ala Trp Glu Pro Thr Gly  
                     35                    40                    45

Thr Arg Ala Leu Lys Pro Pro Pro Gly Pro Glu Thr Asn Gly Glu Asp  
                     50                    55                    60

Pro Leu Pro Ala Cys Thr Pro Ser Pro Gln Asp Leu Lys Glu Leu Glu  
   65                    70                    75                    80

Phe Leu Thr Gln Ala Leu Glu Lys Ala Val Arg Val Arg Arg Gly Ile  
                     85                    90                    95

Thr Lys Ala Glu Glu Arg Asp Lys Ala Pro Ser Leu Lys Ser Arg Ser  
                     100                    105                    110

Ile Val Thr Ser Ser Gly Thr Thr Ala Ser Ala Pro Pro His Ser Pro  
                     115                    120                    125

Gly Gln Ala Gly Gly His Ala Ser Asp Thr Arg Pro Thr Lys Gly Leu  
                     130                    135                    140

Arg Gln Thr Thr Val Pro Ala Lys Gly His Pro Glu Arg Arg Leu Leu  
   145                    150                    155                    160

Ser Val Gly Asp Gly Thr Arg Val Gly Met Gly Ala Arg Thr Pro Arg	165	170	175
Pro Gly Ala Gly Leu Arg Asp Gln Gln Met Ala Pro Ser Ala Ala Pro	180	185	190
Gln Ala Pro Glu Ala Phe Thr Leu Lys Glu Lys Gly His Leu Leu Arg	195	200	205
Leu Pro Ala Ala Phe Arg Lys Ala Ala Ser Gln Asn Ser Ser Leu Trp	210	215	220
Ala Gln Leu Ser Ser Thr Gln Thr Ser Asp Ser Thr Asp Ala Ala Ala	225	230	235
Ala Lys Thr Gln Phe Leu Gln Asn Met Gln Thr Ala Ser Gly Gly Pro	245	250	255
Gln Pro Arg Leu Ser Ala Val Glu Val Glu Ala Glu Ala Gly Arg Leu	260	265	270
Arg Lys Ala Cys Ser Leu Leu Arg Leu Arg Met Arg Glu Glu Leu Ser	275	280	285
Ala Ala Pro Met Asp Trp Met Gln Glu Tyr Arg Cys Leu Leu Thr Leu	290	295	300
Glu Gly Leu Gln Ala Met Val Gly Gln Cys Leu His Arg Leu Gln Glu	305	310	315
Leu Arg Ala Ala Val Ala Glu Gln Pro Pro Arg Pro Cys Pro Val Gly	325	330	335
Arg Pro Pro Gly Ala Ser Pro Ser Cys Gly Gly Arg Ala Glu Pro Ala	340	345	350
Trp Ser Pro Gln Leu Leu Val Tyr Ser Ser Thr Gln Glu Leu Gln Thr	355	360	365
Leu Ala Ala Leu Lys Leu Arg Val Ala Val Leu Asp Gln Gln Ile His	370	375	380
Leu Glu Lys Val Leu Met Ala Glu Leu Leu Pro Leu Val Ser Ala Ala	385	390	395
Gln Pro Gln Gly Pro Pro Trp Leu Ala Leu Cys Arg Ala Val His Ser	405	410	415

Leu Leu Cys Glu Gly Gly Ala Arg Val Leu Thr Ile Leu Arg Asp Glu  
420 425 430

Pro Ala Val  
435

<210> 15  
<211> 513  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(510)

<400> 15  
atg cag gct caa cag tac cag cag cag cgt cga aaa ttt gca gct gcc 48  
Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala  
1 5 10 15  
  
ttc ttg gca ttc att ttc ata ctg gca gct gtg gat act gct gaa gca 96  
Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala  
20 25 30  
  
ggg aag aaa gag aaa cca gaa aaa aaa gtg aag aag tct gac tgt gga 144  
Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly  
35 40 45  
  
gaa tgg cag tgg agt gtg tgt gtg ccc acc agt gga gac tgt ggg ctg 192  
Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu  
50 55 60  
  
ggc aca cgg gag ggc act cgg act gga gct gag tgc aag caa acc atg 240  
Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met  
65 70 75 80  
  
aag acc cag aga tgt aag atc ccc tgc aac tgg aag aag caa ttt ggc 288  
Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly  
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gcg gag tgc aaa tac cag ttc cag gcc tgg gga gaa tgt gac ctg aac 336  
Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn  
100 105 110  
  
aca gcc ctg aag acc aga act gga agt ctg aag cga gcc ctg cac aat 384

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn  
 115 120 125  
  
 gcc gaa tgc cag aag act gtc acc atc tcc aag ccc tgt ggc aaa ctg 432  
 Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu  
 130 135 140  
  
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 Thr Lys Pro Lys Pro Gln Gly Thr Leu Glu Leu Lys Val Lys Lys Lys  
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 Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly  
 35 40 45  
  
 Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu  
 50 55 60  
  
 Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met  
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 85 90 95  
  
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 Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu  
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Lys Lys Lys Lys Asn Ser Glu Glu Thr Phe  
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 <222> (16)..(297)

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 Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe  
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cta tat gaa aag gaa cac atc tgc tgc tta gaa gag tgg acc agc cct 147  
 Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro  
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 Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu  
 45 50 55 60

ctg cct ctt atg gaa gaa gaa acg agc tgt cat tat gat ggt gac agt 243  
 Leu Pro Leu Met Glu Glu Glu Thr Ser Cys His Tyr Asp Gly Asp Ser  
 65 70 75

ggg ggc tct ctt tgc tgt gtg ctg ggc acc att cca tgt tgt cca tat 291  
 Gly Gly Ser Leu Cys Cys Val Leu Gly Thr Ile Pro Cys Cys Pro Tyr  
 80 85 90

gat gat tgaatacagt aattttgaaa aggaatatga tgatgtcaca atcaagatga 347  
 Asp Asp

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432

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<213> Homo sapiens

<400> 18  
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Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro Val His Gln Lys  
35 40 45  
Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu Leu Pro Leu Met  
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Cys Cys Val Leu Gly Thr Ile Pro Cys Cys Pro Tyr Asp Asp  
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<212> DNA  
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<220>  
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<222> (31)..(1395)

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Ser Ala Val Phe Leu Ile Ser Phe Leu Trp Asp Leu Pro Gly Phe Gln  
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Lys	Gly	Met	Arg	Ser	Arg	Lys	Glu	Gly	Lys	Met	Gln	Arg	Ala	Pro	Arg	
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gac	agt	gac	gcg	ggc	cgg	gag	ggc	cag	gaa	cca	cag	ccg	cgg	cct	cag	246
Asp	Ser	Asp	Ala	Gly	Arg	Glu	Gly	Gln	Glu	Pro	Gln	Pro	Arg	Pro	Gln	
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gac	gaa	ccc	cgg	gct	cag	cag	ccc	cgg	gcg	cag	gag	ccg	cca	ggc	agg	294
Asp	Glu	Pro	Arg	Ala	Gln	Gln	Pro	Arg	Ala	Gln	Glu	Pro	Pro	Gly	Arg	
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ggc	ccg	cgc	gtg	gtg	ccc	cac	gag	tac	atg	ctg	tca	atc	tac	agg	act	342
Gly	Pro	Arg	Val	Val	Pro	His	Glu	Tyr	Met	Leu	Ser	Ile	Tyr	Arg	Thr	
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tac	tcc	atc	gct	gag	aag	ctg	ggc	atc	aat	gcc	agc	ttt	ttc	cag	tct	390
Tyr	Ser	Ile	Ala	Glu	Lys	Leu	Gly	Ile	Asn	Ala	Ser	Phe	Phe	Gln	Ser	
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Ser	Lys	Ser	Ala	Asn	Thr	Ile	Thr	Ser	Phe	Val	Asp	Arg	Gly	Leu	Asp	
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gat	ctc	tcg	cac	act	cct	ctc	cgg	aga	cag	aag	tat	ttg	ttt	gat	gtg	486
Asp	Leu	Ser	His	Thr	Pro	Leu	Arg	Arg	Gln	Lys	Tyr	Leu	Phe	Asp	Val	
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tcc	atg	ctc	tca	gac	aaa	gaa	gag	ctg	gtg	ggc	gcg	gag	ctg	cgg	ctc	534
Ser	Met	Leu	Ser	Asp	Lys	Glu	Glu	Leu	Val	Gly	Ala	Glu	Leu	Arg	Leu	
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Phe	Arg	Gln	Ala	Pro	Ser	Ala	Pro	Trp	Gly	Pro	Pro	Ala	Gly	Pro	Leu	
	170					175					180					
cac	gtg	cag	ctc	ttc	cct	tgc	ctt	tcg	ccc	cta	ctg	ctg	gac	gcg	cgg	630
His	Val	Gln	Leu	Phe	Pro	Cys	Leu	Ser	Pro	Leu	Leu	Leu	Asp	Ala	Arg	
185					190					195				200		
acc	ctg	gac	ccg	cag	ggg	gcg	ccg	ccg	gcc	ggc	tgg	gaa	gtc	ttc	gac	678
Thr	Leu	Asp	Pro	Gln	Gly	Ala	Pro	Pro	Ala	Gly	Trp	Glu	Val	Phe	Asp	
			205					210					215			
gtg	tgg	cag	ggc	ctg	cgc	cac	cag	ccc	tgg	aag	cag	ctg	tgc	ttg	gag	726



Val	Trp	Gln	Gly	Leu	Arg	His	Gln	Pro	Trp	Lys	Gln	Leu	Cys	Leu	Glu		
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Leu	Arg	Ala	Ala	Trp	Gly	Glu	Leu	Asp	Ala	Gly	Glu	Ala	Glu	Ala	Arg		
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Phe	Gly	Arg	Arg	Val	Arg	Pro	Pro	Gln	Glu	Arg	Ala	Leu	Leu	Val	Val		
265					270					275					280		
ttc	acc	aga	tcc	cag	cgc	aag	aac	ctg	ttc	gca	gag	atg	cgc	gag	cag	918	
Phe	Thr	Arg	Ser	Gln	Arg	Lys	Asn	Leu	Phe	Ala	Glu	Met	Arg	Glu	Gln		
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Trp	Pro	Pro	Pro	Ser	Gly	Ala	Pro	Asp	Ala	Arg	Pro	Trp	Leu	Pro	Ser		
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Pro	Gly	Arg	Arg	Arg	Arg	Arg	Thr	Ala	Phe	Ala	Ser	Arg	His	Gly	Lys		
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cgg	cac	ggc	aag	aag	tcc	agg	cta	cgc	tgc	agc	aag	aag	ccc	ctg	cac	1110	
Arg	His	Gly	Lys	Lys	Ser	Arg	Leu	Arg	Cys	Ser	Lys	Lys	Pro	Leu	His		
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gtg	aac	ttc	aag	gag	ctg	ggc	tgg	gac	gac	tgg	att	atc	gcg	ccc	ctg	1158	
Val	Asn	Phe	Lys	Glu	Leu	Gly	Trp	Asp	Asp	Trp	Ile	Ile	Ala	Pro	Leu		
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gag	tac	gag	gcc	tat	cac	tgc	gag	ggt	gta	tgc	gac	ttc	ccg	ctg	cgc	1206	
Glu	Tyr	Glu	Ala	Tyr	His	Cys	Glu	Gly	Val	Cys	Asp	Phe	Pro	Leu	Arg		
			380					385				390					
tcg	cac	ctg	gag	ccc	acc	aac	cac	gcc	atc	atc	cag	acg	ctg	atg	aac	1254	
Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	Ile	Ile	Gln	Thr	Leu	Met	Asn		
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Leu Thr Pro Ile Ser Ile Leu Tyr Ile Asp Ala Gly Asn Asn Val Val  
425 430 435 440

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<213> Homo sapiens

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Ser Ser Ala Glu Leu Gly Ser Thr Lys Gly Met Arg Ser Arg Lys Glu  
35 40 45

Gly Lys Met Gln Arg Ala Pro Arg Asp Ser Asp Ala Gly Arg Glu Gly  
50 55 60

Gln Glu Pro Gln Pro Arg Pro Gln Asp Glu Pro Arg Ala Gln Gln Pro  
65 70 75 80

Arg Ala Gln Glu Pro Pro Gly Arg Gly Pro Arg Val Val Pro His Glu  
85 90 95

Tyr Met Leu Ser Ile Tyr Arg Thr Tyr Ser Ile Ala Glu Lys Leu Gly  
100 105 110

Ile Asn Ala Ser Phe Phe Gln Ser Ser Lys Ser Ala Asn Thr Ile Thr  
115 120 125

Ser Phe Val Asp Arg Gly Leu Asp Asp Leu Ser His Thr Pro Leu Arg  
130 135 140

Arg Gln Lys Tyr Leu Phe Asp Val Ser Met Leu Ser Asp Lys Glu Glu

145		150		155		160
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Trp Gly Pro Pro Ala Gly Pro Leu His Val Gln Leu Phe Pro Cys Leu						
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Ser Pro Leu Leu Leu Asp Ala Arg Thr Leu Asp Pro Gln Gly Ala Pro						
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Pro Ala Gly Trp Glu Val Phe Asp Val Trp Gln Gly Leu Arg His Gln						
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Pro Trp Lys Gln Leu Cys Leu Glu Leu Arg Ala Ala Trp Gly Glu Leu						
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Asp Ala Gly Glu Ala Glu Ala Arg Ala Arg Gly Pro Gln Gln Pro Pro						
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Pro Pro Asp Leu Arg Ser Leu Gly Phe Gly Arg Arg Val Arg Pro Pro						
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Gln Glu Arg Ala Leu Leu Val Val Phe Thr Arg Ser Gln Arg Lys Asn						
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Leu Phe Ala Glu Met Arg Glu Gln Leu Gly Ser Ala Glu Ala Ala Gly						
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Pro Gly Ala Gly Ala Glu Gly Ser Trp Pro Pro Pro Ser Gly Ala Pro						
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Asp Ala Arg Pro Trp Leu Pro Ser Pro Gly Arg Arg Arg Arg Arg Thr						
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Ala Phe Ala Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg Leu						
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Arg Cys Ser Lys Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp						
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Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu						
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Gly Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His						
	385		390		395	400
Ala Ile Ile Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro						

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Pro Ser Cys Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr		
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Val Glu Ser Cys Gly Cys Arg		
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<210> 21  
 <211> 1852  
 <212> DNA  
 <213> Homo sapiens

<400> 21

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<210> 22  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence:Forward Primer  
Ag 390

<400> 22  
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<210> 23  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Reverse Primer  
Ag 390

<400> 23  
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<210> 24  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Probe Primer  
Ag390

<400> 24  
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<210> 25  
<211> 379  
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<210> 26  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence:Forward Primer  
Ag 271

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<210> 27  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence:Reverse Primer  
Ag 271

<400> 27  
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<210> 28  
<211> 26  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:Probe Primer Ag  
271

<400> 28  
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<210> 29  
<211> 234  
<212> DNA  
<213> Homo sapiens

<400> 29  
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<210> 30  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence:Forward Primer  
Ag 72

<400> 30  
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<210> 31  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Reverse Primer  
Ag 72

<400> 31  
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<210> 32  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Probe Primer Ag  
72

<400> 32  
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<210> 33  
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<212> DNA  
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<210> 34  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence:Forward Primer  
Ag 248

<400> 34  
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<210> 35  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Reverse Primer  
Ag 248

<400> 35  
aggtagcccg cgcagag 17

<210> 36  
<211> 24



<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Probe Primer Ag  
248

<400> 36

cgtgtacggg ggcacatct cccc

24

<210> 37

<211> 410

<212> DNA

<213> Homo sapiens

<400> 37

tgtcattgtc cttttaccta ttatatTTTT tcatactctg tgaaaacaaa tcagttgccg 60  
gactaacat gacctatgat ggaaataatc cagtacatc tcatagagat gtgccacttt 120  
cttattgcaa ctgagactgc aattgtgatg aaagtcagtg ggaaccagtc tgtgggaaca 180  
atggaataac ttacctgtca cttgtctag caggatgcaa atcctcaagt ggtattaaaa 240  
agcatacagt gttttataac ttagtatttg tggaagtaac tggctctccag aacagaaatt 300  
actcagcgca cttgggtgaa tgcccaagag ataatacttg tacaaggaaa tttttcatct 360  
atgttgcaat tcaagtcata aactctttgt tctctgcaac aggaggtacc 410

<210> 38

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Forward Primer  
Ag 287

<400> 38

aactcagact gcaattgtga tgaaa

25

<210> 39

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Reverse Primer  
Ag 287

<400> 39  
ctagacaagg tgacaggtaa gttattcc 28

<210> 40  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Probe Primer Ag  
287

<400> 40  
ttgttcccac agactgggtc ccactgt 27

<210> 41  
<211> 322  
<212> DNA  
<213> Homo sapiens

<400> 41  
tggcagccct ggaggagccg atggtggacc tggacggcga gctgcctttc gtgcggcccc 60  
tgccccacat tgccgtgctc caggacgagc tgccgcaact cttccaggat gacgacgtcg 120  
gggcccgatga ggaagaggca gagttgcggg gcgaacacac gctcacagag aagtttgtct 180  
gcctggatga ctcttttggc catgactgca gcttgacctg tgatgactgc aggaacggag 240  
ggacctgcct cctgggcctg gatggctgtg attgccccga ggggtggact ggggttattt 300  
gcaatgagat ttgtcctccg ga 322

<210> 42  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Forward Primer  
Ag 252

<400> 42  
gagctgccgc aactcttcc 19

<210> 43  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Reverse Primer

Ag 252

<400> 43

gacaaacttc tctgtgagcg tgtg

24

<210> 44

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Probe Primer Ag

252

<400> 44

cgcaactctg cctcttcctc atcgg

25

<210> 45

<211> 1332

<212> DNA

<213> Homo sapiens

<400> 45

cgccctcatg ctgccggcgg gctgctcgg ccggctggtg gccgagctgc agggcgccct 60  
ggacgcctgc gcacagcgac aattgcaatt ggagcagagc ctgcgcgttt gccgtcggct 120  
gctgcatgcc tgggaaccaa ctgggacccg ggctttgaag ccacctccag ggccagaaac 180  
taatggagag gaccccttc cagcatgcac acccagtcca caagacctca aagagttgga 240  
gtttctgacc caggcactgg agaaggctgt acgagttcga agaggcatca ctaaggccga 300  
agagagagac aaggccccca gcctgaaatc taggtccatt gtcacctctt ctggcacgac 360  
agcctccgcc ccaccgcatt ccccaggcca agctggtggc catgcttcag acacgagacc 420  
caccaagggc ctccgccaga ccacggtgcc tgccaagggc cacctgagc gccggctgct 480  
gtcagtgggg gatgggaccc gtgttgggat gggagcccga acccccaggc ctggggcggg 540  
cctcaggggac cagcaaattg ccccatccgc tgctcctcag gccccagaag ccttcacact 600  
caaggagaag gggcacctgc tgcggctgcc tgcggcattc aggaaagcag cttcccagaa 660  
ctcgagcctg tgggcccagc tcagttccac acagaccagt gattccacgg atgccgccgc 720  
tgccaaaacc cagttcctcc agaacatgca gacagcttca ggcgggcccc agcccaggct 780  
cagtgtgtg gaggtggagg cggaggcggg gcgcctgcgg aaggcctgct cgctgctgag 840  
actgcgcatg agggaggagc tctcagcagc ccccatggac tggatgcagg agtaccgctg 900  
cctgtctacg ctggaggggc tgcaggccat ggtgggccag tgtctgcaca ggctgcagga 960  
gctgcgtgca gcggtggcgg aacagccacc aagaccatgt cctgtgggga gggcccccg 1020  
agcctcgccg tcctgtgggg gtagagcgga gcctgcatgg agccccagc tgcttgtcta 1080  
ctccagcacc caggagctgc agaccctggc ggccctcaag ctgcgagtgg ctgtgctgga 1140  
ccagcagatc cacttggaag aggtcctgat ggctgaactc ctccccctgg taagcgctgc 1200

acagccgcag gggccgccct ggctggccct gtgccgggct gtgcacagcc tgctctgcga 1260  
 gggaggagca cgtgtcctta ccatactgcg ggatgaacct gcagtctgag cctttcccat 1320  
 gctgccctcg gc 1332

<210> 46  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Forward Primer  
 Ab16

<400> 46  
 ggcatcagg aaagcagctt 20

<210> 47  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Reverse Primer  
 Ab16

<400> 47  
 gcatccgtgg aatcactggt 20

<210> 48  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Probe Primer  
 Ab16

<400> 48  
 tgggcccagc tcagttccac aca 23

<210> 49  
 <211> 513  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
atgcaggctc aacagtacca gcagcagcgt cgaaaatttg cagctgcctt cttggcattc 60  
attttcatac tggcagctgt ggatactgct gaagcagga agaaagagaa accagaaaaa 120  
aaagtgaaga agtctgactg tggagaatgg cagtggagtg tgtgtgtgcc caccagtgga 180  
gactgtgggc tgggcacacg ggagggcact cggactggag ctgagtgcaa gcaaaccatg 240  
aagacccaga gatgtaagat cccctgcaac tggagaagc aatttggcgc ggagtgcaaa 300  
taccagtcc aggcctgggg agaatgtgac ctgaacacag ccctgaagac cagaactgga 360  
agtctgaagc gagccctgca caatgccgaa tgccagaaga ctgtcaccat ctccaagccc 420  
tgtggcaaac tgaccaagcc caaacctcaa ggtaccctag aacttaaagt aaaaaaaaaa 480  
aaaaaaaaaa aaaattctga ggagacctt tag 513

<210> 50  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Forward Primer  
Ag 177

<400> 50  
ccctgcacaa tgccgaat 18

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Forward Primer  
Ag 177

<400> 51  
tgaggtttgg gcttggtcag 20

<210> 52  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Forward Primer  
Ag 177

<400> 52  
caccatctcc aagccctgtg gcaa

24

<210> 53  
<211> 432  
<212> DNA  
<213> Homo sapiens

<400> 53  
tttttgaagt ttctattcat aaatgcatag acaatgggat tacagatgga gttggaaaat 60  
ccaataattt gcacgatagc aaaaatcatc ttgattgtga catcatcata ttccttttca 120  
aaattactgt attcaatcat catatggaca acatggaatg gtgccagca cacagcaaag 180  
agagccacca ctgtcaccat cataatgaca gctcgtttct tcttcataa gaggcaggag 240  
gaagaggatg acaaggatga aggtggtgta gatcttctgg tgcacagggc tggtcactc 300  
ttctaagcag cagatgtgtt ccttttcata taggaagtca tatttgatct caagttgttg 360  
cacgtgccac atgggtgatc ctacgatgac tgccaccagc cagaccacac ctagcattgt 420  
gaaagccctt cg 432

<210> 54  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Forward Primer  
GPCR 13

<400> 54  
atggaatggt gccagca 18

<210> 55  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Reverse Primer  
GPCR 13

<400> 55  
tggaagaaga aacgagctgt ca 22

<210> 56  
<211> 27

<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Probe Primer  
GPCR 13

<400> 56  
cagcaaagag agccaccact gtcacca

27

<210> 57  
<211> 102  
<212> DNA  
<213> Homo sapiens

<220>

<221> misc\_feature  
<222> (1)..(2)  
<223> Wherein n is a or t or g or c.

<220>

<221> misc\_feature  
<222> (101)..(102)  
<223> Wherein n is t or a or g or c.

<400> 57  
nngacttact ccacgctga gaagctgggc atcaatgcc a gctttttcca gtcttccaag 60  
tcggctaata cgatcaccag cttttagac aggggactag nn 102

<210> 58  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Forward Primer  
Ag 191

<400> 58  
gacttactcc atcgctgaga agct

24

<210> 59  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Reverse Primer  
Ag 191

<400> 59

gctggtgatc gtattagccg a 21

<210> 60

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Probe Primer Ag  
191

<400> 60

catcaatgcc agctttttcc agtcttcc 28

<210> 61

<211> 238

<212> DNA

<213> Mus musculus

<220>

<221> misc\_feature

<222> (104)

<223> Wherein n is t or a or g or c.

<400> 61

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gagtccggtg tgtggacact gacgagtgtc ccatcggaac ccctgctggg aacgggacat 120  
gcaccaacgt gatcgggtgc ttcgaatgca cctgcaacga aggctttgag ccggggccca 180  
tgatgaactg cgaagacatc aacgagtgtg ccgagaacct gctgctctgt gctttccg 238

<210> 62

<211> 197

<212> DNA

<213> Mus musculus

<400> 62

aagccatgca acttcatctg caagaacacc aagggcagtt accagtgtct ctgcccacgg 60  
gggtacgtcc tgcaggagga cggaaagacg tgcaaagacc tgcacgaatg tcaaaccaaa 120  
cagcacaact gccagttcct ctgtgtcaac accctggggg gattcacctg taaatgtccg 180



ccccggtttca cccagca

197

<210> 63  
<211> 492  
<212> PRT  
<213> Homo sapiens

<400> 63  
Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu  
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Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val  
20 25 30  
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro  
35 40 45  
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val  
50 55 60  
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys  
65 70 75 80  
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val  
85 90 95  
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys  
100 105 110  
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn  
115 120 125  
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp  
130 135 140  
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met  
145 150 155 160  
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp  
165 170 175  
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn  
180 185 190  
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser  
195 200 205

Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys  
210 215 220  
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg  
225 230 235 240  
Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile  
245 250 255  
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser  
260 265 270  
Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro  
275 280 285  
Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn  
290 295 300  
Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met  
305 310 315 320  
Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn  
325 330 335  
Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln  
340 345 350  
Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn  
355 360 365  
Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp  
370 375 380  
Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala  
385 390 395 400  
Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr  
405 410 415  
Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly  
420 425 430  
Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser  
435 440 445  
Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly  
450 455 460

Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe  
 465 470 475 480

Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asp Gly  
 485 490

<210> 64  
 <211> 2656  
 <212> DNA  
 <213> Homo sapiens

<400> 64  
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 cgtgttgtct ttacctgcca ggccacagcc aaccccgaga tcttgggcta caggtgggccc 180  
 aaaggggggtt tcttgattga agacgcccac gagagtcgct atgagacaaa tgtggatttat 240  
 tcctttttca cggagcctgt gtcttgtgag gttcacaaca aagtgggaag caccaatgtc 300  
 agcacttttag taaatgtcca ctttgctccc cggattgtag ttgaccccaa acccacaacc 360  
 acagacattg gctctgatgt gacccttacc tgtgtctggg ttgggaatcc cccctcact 420  
 ctcacctgga ccaaaaagga ctcaaatatg gggcccaggc ctcctggctc cccaccgag 480  
 gctgctctct ctgcccaggt cctgagtaac agcaaccagc tgctgctgaa gtcgggtgact 540  
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 cgccgcaaag gcagtcgcaa agacgtgacc ctgaggaagc tggatatcaa ggtggagaca 1080  
 gtgaaccgag agccacttac gatgcattct gaccgggagg atgacaccgc cagcgtctcc 1140  
 acagcaaccc gggatcatgaa ggccatctac tcgtcggtta aggatgatgt ggatctgaag 1200  
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 aatggctact acaacgtgcg tgcccatgaa gaccgcccgt cttccagggc agtgctctat 1320  
 gctgactacc gtgcccctgg ccctgcccgc ttcgacggcc gccctcatc ccgtctctcc 1380  
 cactccagcg gctatgccc gctcaacacc tatagccggg gccctgctc tgactatggc 1440  
 cctgagccca caccctctgg ccctgctgcc ccagctggca ctgacacaa cagccagctg 1500  
 tcctacgaga actatgagaa gttcaactcc catcccttcc ctggggcagc tgggtacccc 1560  
 acctaccgac tgggctaccc ccaggcccca ccctctggcc tggagcggac cccatatgag 1620  
 gcgtatgacc ccattggcaa gtacgccaca gccactcgat tctcctacac ctcccagcac 1680  
 tcggactacg gccagcgatt ccagcagcgc atgcagactc acgtgtaggg gccagagcct 1740  
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 gggcattgct cattgtctcc ttctcgacc agccttcttc ctcccaccat ggcaggtggg 1860  
 gagcaggtct cccagaaaca cccgtcccg aggatgggtgc tctgtgcatg cccagcctc 1920  
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 tgaccctaga atggggacag ggaaagtgaa ggtagggaa agcagagggg ggcacttttt 2040  
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gatgggcagg ctttggccta gggacatgaa gtatgggagt gggaggctgt ggcacagaca 2160  
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tctctccttc ctcagggtag tgcagaaggg agcgaacagg gtactgttcg ctcttgtcta 2280  
cagaacagcc ctggcactgc attcaaattcc agtcttcatt cagctgggat caaaatgcc 2340  
gtcaccttgg ctaccactg tggacagctg tctgtcagca tgcagaggga tccaggaatc 2400  
cccccgag cagggccgc tttccttctc ctccatgctg ggccagccag ataagtcagg 2460  
gtcctgggtgg agaaagaaag gctaggacca tgtcctcatt gacccagata ctgctgtgtg 2520  
ctgcacagca gtgaaccaac actagaggga gccacacaag cctcctctcc ccagtctgcc 2580  
ccacttctg gctttaactc ttgagctggg ttggggagtg gtgaggtagg ggtgggggtg 2640  
ctgtaggctc tttttc 2656

<210> 65

<211> 1011

<212> PRT

<213> *Drosophila melanogaster*

<400> 65

Met Ala Leu Arg Gln Ser Ala Lys Asp Val Ala Lys Ser Asn Cys Val  
1 5 10 15

Ala Val Arg Ser Ser Ile Ser Leu Ser Leu Val Leu Val Leu Cys Leu  
20 25 30

Ala Leu Val Asp Ser Ser Thr Ala Gln Val Asp Thr Thr Ile Ser Gln  
35 40 45

Gln Glu Ser Gln Ser Val Val Leu Pro Cys Pro Val Asp Ala Glu Lys  
50 55 60

Cys Gly Lys Leu His Ser Leu Asn Trp Phe Lys Gly Asp Asp Arg Ile  
65 70 75 80

Ala Ala Met Leu Leu Gly Asp Ser Asn Val Thr Ser Val Asn Lys Glu  
85 90 95

Phe Asp Glu Arg Val Thr Val Glu Gln Asn Pro Tyr Arg Leu Val Ile  
100 105 110

Lys Asp Leu Lys Ile Ala Asp Glu Asp Ile Tyr Leu Cys Asp Thr Thr  
115 120 125

Phe Phe Ile Pro Glu Glu Thr Cys Asp Asn Phe Asn Gly Tyr Arg Ile  
130 135 140

Glu Leu Arg Val Leu Val Pro Pro Thr Glu Val Val Ile Leu Asp Ala  
145 150 155 160

Lys Gly Asp Arg Ile Lys Asn Gly Ser Val Val Gly Pro Met Gln Glu  
 165 170 175

Arg Gln Ser Leu Lys Ala Thr Cys Thr Val Arg Asn Thr Arg Pro Gln  
 180 185 190

Pro Glu Val Ser Trp Phe Arg Gly Thr Lys Arg Leu Thr Thr Tyr Ser  
 195 200 205

Pro Thr His Asp Leu Val Asp Gly Leu Tyr Thr Ser Thr Leu Glu Leu  
 210 215 220

Asp Trp Thr Leu Ser Arg Glu Asp Leu Ala Gln Asp Ile Glu Cys Arg  
 225 230 235 240

Val Lys Ser Ala Ala Ile Gln Asn Val Thr Val Thr Lys Phe Ser Val  
 245 250 255

Asp Leu Gln Val Arg Pro Thr Ser Ile Asp Ile Asn Gly Val Lys His  
 260 265 270

His Thr Val Gln Gly Ser Lys Val Val Leu Thr Cys Asp Ile His Gly  
 275 280 285

Ala Arg Pro Ala Val Asn Leu Thr Trp Tyr Asn Thr Thr Thr Ile Ile  
 290 295 300

Ser Ser Gly Glu Asn Glu Ile Thr Glu Val Arg Ser Lys Ser Leu Glu  
 305 310 315 320

Lys Ser Asp Gly Thr Phe His Thr Gln Ser Glu Leu Ile Phe Asn Ala  
 325 330 335

Thr Arg Phe Glu Asn Asp Arg Val Phe Arg Cys Glu Ala Glu Asn Ile  
 340 345 350

Val Leu Gln Ile Asn Arg Glu Lys Pro Ile Ser Ser Ala Leu Thr Leu  
 355 360 365

Glu Val Leu Tyr Pro Pro Val Val Lys Val Ser Pro Ser Ala Ile Thr  
 370 375 380

Ala Asn Thr Ser Glu Ile Val Leu Leu Asn Cys Glu Tyr Phe Ala Asn  
 385 390 395 400

Pro Ala Ser Leu Thr Gln Val Glu Trp Tyr Arg Asn Asp Ile Leu Val  
 405 410 415

Asn Val Asn Asp Thr Thr His Tyr Lys Gly Gly Asn Ser Glu Asn Val		
420	425	430
Ala Leu Val Ile Lys Ser Thr Glu Lys Glu Asp Ile Gly Asn Tyr Ser		
435	440	445
Cys Gln Leu Ser Asn Asn Ile Gly Lys Gly Thr Ser Asp Gln Lys Ile		
450	455	460
Asn Leu Asp Val Gln Tyr Ala Pro Thr Val Glu Ile Leu Met Ile Pro		
465	470	475 480
Glu Gly Pro Val Lys Glu Ser Asp Glu Ser Asn Val Thr Leu Phe Cys		
485	490	495
Asn Val Leu Asp Ala Asn Pro Ser Val Leu Thr Lys Val Arg Trp Tyr		
500	505	510
Ala Asn Ser Thr Leu Leu Lys Glu Leu Pro Asp Cys Glu Glu Thr Arg		
515	520	525
Glu Asp Leu Cys His Ile Asp Pro Ser Lys Leu Leu Leu Glu Ser Ile		
530	535	540
Gly Arg Gly Phe Phe Tyr Asn Tyr Ser Cys Glu Gly Phe Asn Ala Ala		
545	550	555 560
Gly Trp Gly Pro Arg Ser Glu Asp Lys Glu Leu Leu Val His Tyr Glu		
565	570	575
Pro Gly Pro Ala Ala Leu Ser His Phe Pro Leu Val Ala Val Lys Lys		
580	585	590
Lys Ser Val Thr Phe Ser Cys Ser Val Asp Asp Pro Gly Phe Pro Glu		
595	600	605
Ser Asn Arg Phe Arg Trp Leu Arg Gly Gly Arg Gly Pro Leu Gln Asp		
610	615	620
Ile Val Thr Lys Asp Trp Thr Val Glu Pro Val Gly Leu Asp Ser Arg		
625	630	635 640
Thr Asn Tyr Ser Cys Tyr Ala Tyr Asn Glu Gly Gly Lys Gly Val Met		
645	650	655
Ala Thr Val Asn Leu Glu Val His Ala Pro Pro Phe Phe Ile Lys Asn		
660	665	670

Leu Pro Pro Tyr Thr Gly Ile Leu His Ser Ser Pro Asn Ala Thr Leu  
 675 680 685

Thr Cys Arg Ile Glu Cys Val Pro Arg Cys Asp Ile Ser Trp Gln Lys  
 690 695 700

Asp Gly Val Pro Ile Glu Arg Asn Asp Ser Arg Tyr Phe Ile Lys Glu  
 705 710 715 720

Asn Thr Trp Met Pro Pro Pro Gln Arg Glu Ile Leu Lys Ser Met Leu  
 725 730 735

Ser Val Leu His Phe Asn Met Pro Asn Trp Pro Asp Ser Lys Phe Asn  
 740 745 750

Ile Glu Ala Asp Asn Ala Asn Tyr Ser Cys Val Ser Thr Gly Asn Ile  
 755 760 765

Val Gly Gly Ser Ile Arg Ser Arg Thr Tyr Tyr Phe Gly Ile Glu Ala  
 770 775 780

Pro Glu Asn Thr Thr Val Ser Glu Asn Ile Val Tyr Val Gln Glu Asp  
 785 790 795 800

Thr Ile Pro Gly Arg Val Ile Cys Lys Ser Arg Ala Asn Pro Glu Pro  
 805 810 815

Ser Tyr Lys Trp Ile Phe Lys Asn Glu Thr Ile Ala Asn Gly Asn Ala  
 820 825 830

Leu Ile Ile Asn Thr Ala Met Asn Arg Asn Asp Asp Gly Thr Tyr Thr  
 835 840 845

Cys Leu Ala Tyr Asn Lys His Gly Ser Ser Ile Ala Lys Thr Val Ile  
 850 855 860

Lys Val Gln Phe Lys Pro Arg Cys Glu Ile Glu Arg Gln Glu Ile Asp  
 865 870 875 880

Asp Gln Asp Thr Leu Ile Cys Thr Ala Tyr Gly Asn Pro Ile Glu Ala  
 885 890 895

Asp Phe Ser Trp Ser Ile Lys Thr Glu Asn Glu Thr Asp Glu Asn Leu  
 900 905 910

Gly Ser Gly Lys Lys Glu Asn Ser Val Glu Lys Ser Phe Tyr Ile Leu  
 915 920 925

Gln Thr Asp Tyr Ala Ile Ser Arg Thr Tyr Arg Cys Val Ala Asn Asn  
 930 935 940

Thr Val Gly Tyr Gly Pro Phe Cys Glu Ile Glu Val Ala Glu Gln Leu  
 945 950 955 960

Ala Trp Trp Gln Leu Trp Glu Lys Asn Thr Leu Ile Ile Leu Val Ala  
 965 970 975

Ala Ile Leu Gly Leu Leu Leu Thr Val Ile Val Ile Cys Cys Ile Ile  
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Ile Cys Ile Cys Arg Pro Val Gly Ala Arg Ile Asn Tyr Thr Thr Ser  
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Arg Leu His  
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<210> 66  
 <211> 862  
 <212> PRT  
 <213> Mus musculus

<400> 66  
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Thr Leu Phe Ala Trp Glu Gly Ala Cys Ile Arg Ile Pro Cys Lys Tyr  
 35 40 45

Lys Thr Pro Leu Pro Lys Ala Arg Leu Asp Asn Ile Leu Leu Phe Gln  
 50 55 60

Asn Tyr Glu Phe Asp Lys Ala Thr Lys Lys Phe Lys Gly Thr Val Leu  
 65 70 75 80

Tyr Asn Lys Ala Glu Pro Glu Leu Tyr Pro Pro Lys Gln Arg Arg Val  
 85 90 95

Thr Phe Leu Gly Asn Ser Ile Asp Asn Cys Thr Leu Lys Ile His Pro  
 100 105 110

Ile Arg Ala Asn Asp Ser Gly Asn Leu Gly Leu Arg Met Thr Ala Gly  
 115 120 125



Thr	Glu	Arg	Trp	Met	Glu	Pro	Ile	His	Leu	Asn	Val	Ser	Glu	Lys	Pro	130	135	140	
Phe	Gln	Pro	Tyr	Ile	Gln	Met	Pro	Ser	Glu	Ile	Arg	Glu	Ser	Gln	Ser	145	150	155	160
Val	Thr	Leu	Thr	Cys	Gly	Leu	Asn	Phe	Ser	Cys	Phe	Glu	Tyr	Asp	Ile	165	170	175	
Leu	Leu	Gln	Trp	Phe	Leu	Glu	Asp	Ser	Lys	Ile	Thr	Ser	Val	Thr	Pro	180	185	190	
Ser	Val	Thr	Ser	Ile	Thr	Ser	Ser	Val	Thr	Ser	Ser	Ile	Lys	Asn	Val	195	200	205	
Tyr	Thr	Glu	Ser	Lys	Leu	Thr	Phe	Gln	Pro	Lys	Trp	Thr	Asp	His	Gly	210	215	220	
Lys	Ser	Val	Lys	Cys	Gln	Val	Gln	His	Ser	Ser	Glu	Val	Leu	Ser	Glu	225	230	235	240
Arg	Thr	Val	Arg	Leu	Asp	Val	Lys	Tyr	Thr	Pro	Lys	Leu	Glu	Ile	Lys	245	250	255	
Val	Asn	Pro	Thr	Glu	Val	Glu	Lys	Asn	Asn	Ser	Val	Thr	Met	Thr	Cys	260	265	270	
Arg	Val	Asn	Ser	Ser	Asn	Pro	Lys	Leu	Arg	Thr	Val	Ala	Val	Ser	Trp	275	280	285	
Phe	Lys	Asp	Gly	Arg	Pro	Leu	Glu	Asp	Gln	Glu	Leu	Glu	Gln	Glu	Gln	290	295	300	
Gln	Met	Ser	Lys	Leu	Ile	Leu	His	Ser	Val	Thr	Lys	Asp	Met	Arg	Gly	305	310	315	320
Lys	Tyr	Arg	Cys	Gln	Ala	Ser	Asn	Asp	Ile	Gly	Pro	Gly	Glu	Ser	Glu	325	330	335	
Glu	Val	Glu	Leu	Thr	Val	His	Tyr	Ala	Pro	Glu	Pro	Ser	Arg	Val	His	340	345	350	
Ile	Tyr	Pro	Ser	Pro	Ala	Glu	Glu	Gly	Gln	Ser	Val	Glu	Leu	Ile	Cys	355	360	365	
Glu	Ser	Leu	Ala	Ser	Pro	Ser	Ala	Thr	Asn	Tyr	Thr	Trp	Tyr	His	Asn	370	375	380	

Arg Lys Pro Ile Pro Gly Asp Thr Gln Glu Lys Leu Arg Ile Pro Lys			
385	390	395	400
Val Ser Pro Trp His Ala Gly Asn Tyr Ser Cys Leu Ala Glu Asn Arg			
	405	410	415
Leu Gly His Gly Lys Ile Asp Gln Glu Ala Lys Leu Asp Val His Tyr			
	420	425	430
Ala Pro Lys Ala Val Thr Thr Val Ile Gln Ser Phe Thr Pro Ile Leu			
	435	440	445
Glu Gly Asp Ser Val Thr Leu Val Cys Arg Tyr Asn Ser Ser Asn Pro			
	450	455	460
Asp Val Thr Ser Tyr Arg Trp Asn Pro Gln Gly Ser Gly Ser Val Leu			
465	470	475	480
Lys Pro Gly Val Leu Arg Ile Gln Lys Val Thr Trp Asp Ser Met Pro			
	485	490	495
Val Ser Cys Ala Ala Cys Asn His Lys Cys Ser Trp Ala Leu Pro Val			
	500	505	510
Ile Leu Asn Val His Tyr Ala Pro Arg Asp Val Lys Val Leu Lys Val			
	515	520	525
Ser Pro Ala Ser Glu Ile Arg Ala Gly Gln Arg Val Leu Leu Gln Cys			
	530	535	540
Asp Phe Ala Glu Ser Asn Pro Ala Glu Val Arg Phe Phe Trp Lys Lys			
545	550	555	560
Asn Gly Ser Leu Val Gln Glu Gly Arg Tyr Leu Ser Phe Gly Ser Val			
	565	570	575
Ser Pro Glu Asp Ser Gly Asn Tyr Asn Cys Met Val Asn Asn Ser Ile			
	580	585	590
Gly Glu Thr Leu Ser Gln Ala Trp Asn Leu Gln Val Leu Tyr Ala Pro			
	595	600	605
Arg Arg Leu Arg Val Ser Ile Ser Pro Gly Asp His Val Met Glu Gly			
	610	615	620
Lys Lys Ala Thr Leu Ser Cys Glu Ser Asp Ala Asn Pro Pro Ile Ser			
625	630	635	640

Gln Tyr Thr Trp Phe Asp Ser Ser Gly Gln Asp Leu His Ser Ser Gly  
645 650 655

Gln Lys Leu Arg Leu Glu Pro Leu Glu Val Gln His Thr Gly Ser Tyr  
660 665 670

Arg Cys Lys Gly Thr Asn Gly Ile Gly Thr Gly Glu Ser Pro Pro Ser  
675 680 685

Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Lys Arg Val Ala  
690 695 700

Leu Gly Leu Gly Phe Cys Leu Thr Ile Cys Ile Leu Ala Ile Trp Gly  
705 710 715 720

Met Lys Ile Gln Lys Lys Trp Lys Gln Asn Arg Ser Gln Gln Gly Leu  
725 730 735

Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Ala  
740 745 750

Arg Arg Thr Pro Leu Ser Glu Gly Pro Gln Ser Gln Gly Cys Tyr Asn  
755 760 765

Pro Ala Met Asp Asp Thr Val Ser Tyr Ala Ile Leu Arg Phe Pro Glu  
770 775 780

Ser Asp Met His Asn Ala Gly Asp Ala Gly Thr Pro Ala Thr Gln Ala  
785 790 795 800

Pro Pro Pro Asn Asn Ser Asp Ser Val Thr Tyr Ser Val Ile Gln Lys  
805 810 815

Arg Pro Met Gly Asp Tyr Glu Asn Val Asn Pro Ser Cys Pro Glu Asp  
820 825 830

Glu Ser Ile His Tyr Ser Glu Leu Val Gln Phe Gly Ala Gly Lys Arg  
835 840 845

Pro Gln Ala Lys Glu Asp Val Asp Tyr Val Thr Leu Lys His  
850 855 860

<210> 67  
<211> 1399  
<212> DNA  
<213> Homo sapiens

<400> 67

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agggaccccc ctgcctcgtg ccccatgatg cggccacat ggcgcctccg gcctctgccc 180
ccctctcccc acagatatcg acgagtgtcg catctctcct gacctctgcg gccagggcac 240
ctgtgtcaac acgccgggca gctttgagtg cgagtgtttt cccggctacg agagtggctt 300
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caggggagccc tcttttcttg gagctcacag cctaacagga agacagacat gaataacatg 780
aatcgctgag gaaatgcaaa actgggctgg gtgcagtggc cctcgctgtg aatcccagca 840
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gagattctgt ctccaaatt                                     1399
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<210> 68

<211> 2911

<212> PRT

<213> Homo sapiens

<400> 68

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Gly Cys Val Val Leu Trp Ala Gln Gly Thr Ala Gly Gln Pro Gln Pro
      20              25              30

Pro Pro Pro Lys Pro Pro Arg Pro Gln Pro Pro Pro Gln Gln Val Arg
      35              40              45

Ser Ala Thr Ala Gly Ser Glu Gly Gly Phe Leu Ala Pro Glu Tyr Arg
      50              55              60

Glu Glu Gly Ala Ala Val Ala Ser Arg Val Arg Arg Arg Gly Gln Gln
      65              70              75              80
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Asp	Val	Leu	Arg	Gly	Pro	Asn	Val	Cys	Gly	Ser	Arg	Phe	His	Ser	Tyr	85	90	95	
Cys	Cys	Pro	Gly	Trp	Lys	Thr	Leu	Pro	Gly	Gly	Asn	Gln	Cys	Ile	Val	100	105	110	
Pro	Ile	Cys	Arg	Asn	Ser	Cys	Gly	Asp	Gly	Phe	Cys	Ser	Arg	Pro	Asn	115	120	125	
Met	Cys	Thr	Cys	Ser	Ser	Gly	Gln	Ile	Ser	Ser	Thr	Cys	Gly	Ser	Lys	130	135	140	
Ser	Ile	Gln	Gln	Cys	Ser	Val	Arg	Cys	Met	Asn	Gly	Gly	Thr	Cys	Ala	145	150	155	160
Asp	Asp	His	Cys	Gln	Cys	Gln	Lys	Gly	Tyr	Ile	Gly	Thr	Tyr	Cys	Gly	165	170	175	
Gln	Pro	Val	Cys	Glu	Asn	Gly	Cys	Gln	Asn	Gly	Gly	Arg	Cys	Ile	Ala	180	185	190	
Gln	Pro	Cys	Ala	Cys	Val	Tyr	Gly	Phe	Thr	Gly	Pro	Gln	Cys	Glu	Arg	195	200	205	
Asp	Tyr	Arg	Thr	Gly	Pro	Cys	Phe	Thr	Gln	Val	Asn	Asn	Gln	Met	Cys	210	215	220	
Gln	Gly	Gln	Leu	Thr	Gly	Ile	Val	Cys	Thr	Lys	Thr	Leu	Cys	Cys	Ala	225	230	235	240
Thr	Thr	Gly	Arg	Ala	Trp	Gly	His	Pro	Cys	Glu	Met	Cys	Pro	Ala	Gln	245	250	255	
Pro	Gln	Pro	Cys	Arg	Arg	Gly	Phe	Ile	Pro	Asn	Ile	Arg	Thr	Gly	Ala	260	265	270	
Cys	Gln	Asp	Val	Asp	Glu	Cys	Gln	Ala	Ile	Pro	Gly	Ile	Cys	Gln	Gly	275	280	285	
Gly	Asn	Cys	Ile	Asn	Thr	Val	Gly	Ser	Phe	Glu	Cys	Arg	Cys	Pro	Ala	290	295	300	
Gly	His	Lys	Gln	Ser	Glu	Thr	Thr	Gln	Lys	Cys	Glu	Asp	Ile	Asp	Glu	305	310	315	320
Cys	Ser	Ile	Ile	Pro	Gly	Ile	Cys	Glu	Thr	Gly	Glu	Cys	Ser	Asn	Thr	325	330	335	

Val Gly Ser Tyr Phe Cys Val Cys Pro Arg Gly Tyr Val Thr Ser Thr	340	345	350
Asp Gly Ser Arg Cys Ile Asp Gln Arg Thr Gly Met Cys Phe Ser Gly	355	360	365
Leu Val Asn Gly Arg Cys Ala Gln Glu Leu Pro Gly Arg Met Thr Lys	370	375	380
Met Gln Cys Cys Cys Glu Pro Gly Arg Cys Trp Gly Ile Gly Thr Ile	385	390	395
Pro Glu Ala Cys Pro Val Arg Gly Ser Glu Glu Tyr Arg Arg Leu Cys	405	410	415
Met Asp Gly Leu Pro Met Gly Gly Ile Pro Gly Ser Ala Gly Ser Arg	420	425	430
Pro Gly Gly Thr Gly Gly Asn Gly Phe Ala Pro Ser Gly Asn Gly Asn	435	440	445
Gly Tyr Gly Pro Gly Gly Thr Gly Phe Ile Pro Ile Pro Gly Gly Asn	450	455	460
Gly Phe Ser Pro Gly Val Gly Gly Ala Gly Val Gly Ala Gly Gly Gln	465	470	475
Gly Pro Ile Ile Thr Gly Leu Thr Ile Leu Asn Gln Thr Ile Asp Ile	485	490	495
Cys Lys His His Ala Asn Leu Cys Leu Asn Gly Arg Cys Ile Pro Thr	500	505	510
Val Ser Ser Tyr Arg Cys Glu Cys Asn Met Gly Tyr Lys Gln Asp Ala	515	520	525
Asn Gly Asp Cys Ile Asp Val Asp Glu Cys Thr Ser Asn Pro Cys Thr	530	535	540
Asn Gly Asp Cys Val Asn Thr Pro Gly Ser Tyr Tyr Cys Lys Cys His	545	550	555
Ala Gly Phe Gln Arg Thr Pro Thr Lys Gln Ala Cys Ile Asp Ile Asp	565	570	575
Glu Cys Ile Gln Asn Gly Val Leu Cys Lys Asn Gly Arg Cys Val Asn	580	585	590

Ser Asp Gly Ser Phe Gln Cys Ile Cys Asn Ala Gly Phe Glu Leu Thr  
 595 600 605

Thr Asp Gly Lys Asn Cys Val Asp His Asp Glu Cys Thr Thr Thr Asn  
 610 615 620

Met Cys Leu Asn Gly Met Cys Ile Asn Glu Asp Gly Ser Phe Lys Cys  
 625 630 635 640

Ile Cys Lys Pro Gly Phe Val Leu Ala Pro Asn Gly Arg Tyr Cys Thr  
 645 650 655

Asp Val Asp Glu Cys Gln Thr Pro Gly Ile Cys Met Asn Gly His Cys  
 660 665 670

Ile Asn Ser Glu Gly Ser Phe Arg Cys Asp Cys Pro Pro Gly Leu Ala  
 675 680 685

Val Gly Met Asp Gly Arg Val Cys Val Asp Thr His Met Arg Ser Thr  
 690 695 700

Cys Tyr Gly Gly Ile Lys Lys Gly Val Cys Val Arg Pro Phe Pro Gly  
 705 710 715 720

Ala Val Thr Lys Ser Glu Cys Cys Cys Ala Asn Pro Asp Tyr Gly Phe  
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Gly Glu Pro Cys Gln Pro Cys Pro Ala Lys Asn Ser Ala Glu Phe His  
 740 745 750

Gly Leu Cys Ser Ser Gly Val Gly Ile Thr Val Asp Gly Arg Asp Ile  
 755 760 765

Asn Glu Cys Ala Leu Asp Pro Asp Ile Cys Ala Asn Gly Ile Cys Glu  
 770 775 780

Asn Leu Arg Gly Ser Tyr Arg Cys Asn Cys Asn Ser Gly Tyr Glu Pro  
 785 790 795 800

Asp Ala Ser Gly Arg Asn Cys Ile Asp Ile Asp Glu Cys Leu Val Asn  
 805 810 815

Arg Leu Leu Cys Asp Asn Gly Leu Cys Arg Asn Thr Pro Gly Ser Tyr  
 820 825 830

Ser Cys Thr Cys Pro Pro Gly Tyr Val Phe Arg Thr Glu Thr Glu Thr  
 835 840 845

Cys Glu Asp Ile Asn Glu Cys Glu Ser Asn Pro Cys Val Asn Gly Ala  
850 855 860

Cys Arg Asn Asn Leu Gly Ser Phe Asn Cys Glu Cys Ser Pro Gly Ser  
865 870 875 880

Lys Leu Ser Ser Thr Gly Leu Ile Cys Ile Asp Ser Leu Lys Gly Thr  
885 890 895

Cys Trp Leu Asn Ile Gln Asp Ser Arg Cys Glu Val Asn Ile Asn Gly  
900 905 910

Ala Thr Leu Lys Ser Glu Cys Cys Ala Thr Leu Gly Ala Ala Trp Gly  
915 920 925

Ser Pro Cys Glu Arg Cys Glu Leu Asp Thr Ala Cys Pro Arg Gly Leu  
930 935 940

Ala Arg Ile Lys Gly Val Thr Cys Glu Asp Val Asn Glu Cys Glu Val  
945 950 955 960

Phe Pro Gly Val Cys Pro Asn Gly Arg Cys Val Asn Ser Lys Gly Ser  
965 970 975

Phe His Cys Glu Cys Pro Glu Gly Leu Thr Leu Asp Gly Thr Gly Arg  
980 985 990

Val Cys Leu Asp Ile Arg Met Glu Gln Cys Tyr Leu Lys Trp Asp Glu  
995 1000 1005

Asp Glu Cys Ile His Pro Val Pro Gly Lys Phe Arg Met Asp Ala Cys  
1010 1015 1020

Cys Cys Ala Val Gly Ala Ala Trp Gly Thr Glu Cys Glu Glu Cys Pro  
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Lys Pro Gly Thr Lys Glu Tyr Glu Thr Leu Cys Pro Arg Gly Ala Gly  
1045 1050 1055

Phe Ala Asn Arg Gly Asp Val Leu Thr Gly Arg Pro Phe Tyr Lys Asp  
1060 1065 1070

Ile Asn Glu Cys Lys Ala Phe Pro Gly Met Cys Thr Tyr Gly Lys Cys  
1075 1080 1085

Arg Asn Thr Ile Gly Ser Phe Lys Cys Arg Cys Asn Ser Gly Phe Ala  
1090 1095 1100



Leu Asp Met Glu Glu Arg Asn Cys Thr Asp Ile Asp Glu Cys Arg Ile  
 1105 1110 1115 1120

Ser Pro Asp Leu Cys Gly Ser Gly Ile Cys Val Asn Thr Pro Gly Ser  
 1125 1130 1135

Phe Glu Cys Glu Cys Phe Glu Gly Tyr Glu Ser Gly Phe Met Met Met  
 1140 1145 1150

Lys Asn Cys Met Asp Ile Asp Gly Cys Glu Arg Asn Pro Leu Leu Cys  
 1155 1160 1165

Arg Gly Gly Thr Cys Val Asn Thr Glu Gly Ser Phe Gln Cys Asp Cys  
 1170 1175 1180

Pro Leu Gly His Glu Leu Ser Pro Ser Arg Glu Asp Cys Val Asp Ile  
 1185 1190 1195 1200

Asn Glu Cys Ser Leu Ser Asp Asn Leu Cys Arg Asn Gly Lys Cys Val  
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Asn Met Ile Gly Thr Tyr Gln Cys Ser Cys Asn Pro Gly Tyr Gln Ala  
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Thr Pro Asp Arg Gln Gly Cys Thr Asp Ile Asp Glu Cys Met Ile Met  
 1235 1240 1245

Asn Gly Gly Cys Asp Thr Gln Cys Thr Asn Ser Glu Gly Ser Tyr Glu  
 1250 1255 1260

Cys Ser Cys Ser Glu Gly Tyr Ala Leu Met Pro Asp Gly Arg Ser Cys  
 1265 1270 1275 1280

Ala Asp Ile Asp Glu Cys Glu Asn Asn Pro Asp Ile Cys Asp Gly Gly  
 1285 1290 1295

Gln Cys Thr Asn Ile Pro Gly Glu Tyr Arg Cys Leu Cys Tyr Asp Gly  
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Phe Met Ala Ser Met Asp Met Lys Thr Cys Ile Asp Val Asn Glu Cys  
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Asp Leu Asn Ser Asn Ile Cys Met Phe Gly Glu Cys Glu Asn Thr Lys  
 1330 1335 1340

Gly Ser Phe Ile Cys His Cys Gln Leu Gly Tyr Ser Val Lys Lys Gly  
 1345 1350 1355 1360

Thr Thr Gly Cys Thr Asp Val Asp Glu Cys Glu Ile Gly Ala His Asn			
1365	1370	1375	
Cys Asp Met His Ala Ser Cys Leu Asn Ile Pro Gly Ser Phe Lys Cys			
1380	1385	1390	
Ser Cys Arg Glu Gly Trp Ile Gly Asn Gly Ile Lys Cys Ile Asp Leu			
1395	1400	1405	
Asp Glu Cys Ser Asn Gly Thr His Gln Cys Ser Ile Asn Ala Gln Cys			
1410	1415	1420	
Val Asn Thr Pro Gly Ser Tyr Arg Cys Ala Cys Ser Glu Gly Phe Thr			
1425	1430	1435	1440
Gly Asp Gly Phe Thr Cys Ser Asp Val Asp Glu Cys Ala Glu Asn Ile			
1445	1450	1455	
Asn Leu Cys Glu Asn Gly Gln Cys Leu Asn Val Pro Gly Ala Tyr Arg			
1460	1465	1470	
Cys Glu Cys Glu Met Gly Phe Thr Pro Ala Ser Asp Ser Arg Ser Cys			
1475	1480	1485	
Gln Asp Ile Asp Glu Cys Ser Phe Gln Asn Ile Cys Val Ser Gly Thr			
1490	1495	1500	
Cys Asn Asn Leu Pro Gly Met Phe His Cys Ile Cys Asp Asp Gly Tyr			
1505	1510	1515	1520
Glu Leu Asp Arg Thr Gly Gly Asn Cys Thr Asp Ile Asp Glu Cys Ala			
1525	1530	1535	
Asp Pro Ile Asn Cys Val Asn Gly Leu Cys Val Asn Thr Pro Gly Arg			
1540	1545	1550	
Tyr Glu Cys Asn Cys Pro Pro Asp Phe Gln Leu Asn Pro Thr Gly Val			
1555	1560	1565	
Gly Cys Val Asp Asn Arg Val Gly Asn Cys Tyr Leu Lys Phe Gly Pro			
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Arg Gly Asp Gly Ser Leu Ser Cys Asn Thr Glu Ile Gly Val Gly Val			
1585	1590	1595	1600
Ser Arg Ser Ser Cys Cys Cys Ser Leu Gly Lys Ala Trp Gly Asn Pro			
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Cys Glu Thr Cys Pro Pro Val Asn Ser Thr Glu Tyr Tyr Thr Leu Cys			
1620	1625	1630	
Pro Gly Gly Glu Gly Phe Arg Pro Asn Pro Ile Thr Ile Ile Leu Glu			
1635	1640	1645	
Asp Ile Asp Glu Cys Gln Glu Leu Pro Gly Leu Cys Gln Gly Gly Asn			
1650	1655	1660	
Cys Ile Asn Thr Phe Gly Ser Phe Gln Cys Glu Cys Pro Gln Gly Tyr			
1665	1670	1675	1680
Tyr Leu Ser Glu Asp Thr Arg Ile Cys Glu Asp Ile Asp Glu Cys Phe			
1685	1690	1695	
Ala His Pro Gly Val Cys Gly Pro Gly Thr Cys Tyr Asn Thr Leu Gly			
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Asn Tyr Thr Cys Ile Cys Pro Pro Glu Tyr Met Gln Val Asn Gly Gly			
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His Asn Cys Met Asp Met Arg Lys Ser Phe Cys Tyr Arg Ser Tyr Asn			
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Gly Thr Thr Cys Glu Asn Glu Leu Pro Phe Asn Val Thr Lys Arg Met			
1745	1750	1755	1760
Cys Cys Cys Thr Tyr Asn Val Gly Lys Ala Gly Asn Lys Pro Cys Glu			
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Pro Cys Pro Thr Pro Gly Thr Ala Asp Phe Lys Thr Ile Cys Gly Asn			
1780	1785	1790	
Ile Pro Gly Phe Thr Phe Asp Ile His Thr Gly Lys Ala Val Asp Ile			
1795	1800	1805	
Asp Glu Cys Lys Glu Ile Pro Gly Ile Cys Ala Asn Gly Val Cys Ile			
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Asn Gln Ile Gly Ser Phe Arg Cys Glu Cys Pro Thr Gly Phe Ser Tyr			
1825	1830	1835	1840
Asn Asp Leu Leu Leu Val Cys Glu Asp Ile Asp Glu Cys Ser Asn Gly			
1845	1850	1855	
Asp Asn Leu Cys Gln Arg Asn Ala Asp Cys Ile Asn Ser Pro Gly Ser			
1860	1865	1870	

Tyr Arg Cys Glu Cys Ala Ala Gly Phe Lys Leu Ser Pro Asn Gly Ala		
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Cys Val Asp Arg Asn Glu Cys Leu Glu Ile Pro Asn Val Cys Ser His		
1890	1895	1900
Gly Leu Cys Val Asp Leu Gln Gly Ser Tyr Gln Cys Ile Cys His Asn		
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Gly Phe Lys Ala Ser Gln Asp Gln Thr Met Cys Met Asp Val Asp Glu		
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Cys Glu Arg His Pro Cys Gly Asn Gly Thr Cys Lys Asn Thr Val Gly		
1940	1945	1950
Ser Tyr Asn Cys Leu Cys Tyr Pro Gly Phe Glu Leu Thr His Asn Asn		
1955	1960	1965
Asp Cys Leu Asp Ile Asp Glu Cys Ser Ser Phe Phe Gly Gln Val Cys		
1970	1975	1980
Arg Asn Gly Arg Cys Phe Asn Glu Ile Gly Ser Phe Lys Cys Leu Cys		
1985	1990	1995 2000
Asn Glu Gly Tyr Glu Leu Thr Pro Asp Gly Lys Asn Cys Ile Asp Thr		
	2005	2010 2015
Asn Glu Cys Val Ala Leu Pro Gly Ser Cys Ser Pro Gly Thr Cys Gln		
	2020	2025 2030
Asn Leu Glu Gly Ser Phe Arg Cys Ile Cys Pro Pro Gly Tyr Glu Val		
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Lys Ser Glu Asn Cys Ile Asp Ile Asn Glu Cys Asp Glu Asp Pro Asn		
	2050	2055 2060
Ile Cys Leu Phe Gly Ser Cys Thr Asn Thr Pro Gly Gly Phe Gln Cys		
2065	2070	2075 2080
Leu Cys Pro Pro Gly Phe Val Leu Ser Asp Asn Gly Arg Arg Cys Phe		
	2085	2090 2095
Asp Thr Arg Gln Ser Phe Cys Phe Thr Asn Phe Glu Asn Gly Lys Cys		
	2100	2105 2110
Ser Val Pro Lys Ala Phe Asn Thr Thr Lys Ala Lys Cys Cys Cys Ser		
	2115	2120 2125

Lys Met Pro Gly Glu Gly Trp Gly Asp Pro Cys Glu Leu Cys Pro Lys  
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Asp Asp Glu Val Ala Phe Gln Asp Leu Cys Pro Tyr Gly His Gly Thr  
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Val Pro Ser Leu His Asp Thr Arg Glu Asp Val Asn Glu Cys Leu Glu  
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Ser Pro Gly Ile Cys Ser Asn Gly Gln Cys Ile Asn Thr Asp Gly Ser  
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Phe Arg Cys Glu Cys Pro Met Gly Tyr Asn Leu Asp Tyr Thr Gly Val  
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Arg Cys Val Asp Thr Asp Glu Cys Ser Ile Gly Asn Pro Cys Gly Asn  
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Gly Thr Cys Thr Asn Val Ile Gly Ser Phe Glu Cys Asn Cys Asn Glu  
 2225 2230 2235 2240

Gly Phe Glu Pro Gly Pro Met Met Asn Cys Glu Asp Ile Asn Glu Cys  
 2245 2250 2255

Ala Gln Asn Pro Leu Leu Cys Ala Leu Arg Cys Met Asn Thr Phe Gly  
 2260 2265 2270

Ser Tyr Glu Cys Thr Cys Pro Ile Gly Tyr Ala Leu Arg Glu Asp Gln  
 2275 2280 2285

Lys Met Cys Lys Asp Leu Asp Glu Cys Ala Glu Gly Leu His Asp Cys  
 2290 2295 2300

Glu Ser Arg Gly Met Met Cys Lys Asn Leu Ile Gly Thr Phe Met Cys  
 2305 2310 2315 2320

Ile Cys Pro Pro Gly Met Ala Arg Arg Pro Asp Gly Glu Gly Cys Val  
 2325 2330 2335

Asp Glu Asn Glu Cys Arg Thr Lys Pro Gly Ile Cys Glu Asn Gly Arg  
 2340 2345 2350

Cys Val Asn Ile Ile Gly Ser Tyr Arg Cys Glu Cys Asn Glu Gly Phe  
 2355 2360 2365

Gln Ser Ser Ser Ser Gly Thr Glu Cys Leu Asp Asn Arg Gln Gly Leu  
 2370 2375 2380

Cys Phe Ala Glu Val Leu Gln Thr Ile Cys Gln Met Ala Ser Ser Ser  
 2385 2390 2395 2400  
 Arg Asn Leu Val Thr Lys Ser Glu Cys Cys Cys Asp Gly Gly Arg Gly  
 2405 2410 2415  
 Trp Gly His Gln Cys Glu Leu Cys Pro Leu Pro Gly Thr Ala Gln Tyr  
 2420 2425 2430  
 Lys Lys Ile Cys Pro His Gly Pro Gly Tyr Thr Thr Asp Gly Arg Asp  
 2435 2440 2445  
 Ile Asp Glu Cys Lys Val Met Pro Asn Leu Cys Thr Asn Gly Gln Cys  
 2450 2455 2460  
 Ile Asn Thr Met Gly Ser Phe Arg Cys Phe Cys Lys Val Gly Tyr Thr  
 2465 2470 2475 2480  
 Thr Asp Ile Ser Gly Thr Ser Cys Ile Asp Leu Asp Glu Cys Ser Gln  
 2485 2490 2495  
 Ser Pro Lys Pro Cys Asn Tyr Ile Cys Lys Asn Thr Glu Gly Ser Tyr  
 2500 2505 2510  
 Gln Cys Ser Cys Pro Arg Gly Tyr Val Leu Gln Glu Asp Gly Lys Thr  
 2515 2520 2525  
 Cys Lys Asp Leu Asp Glu Cys Gln Thr Lys Gln His Asn Cys Gln Phe  
 2530 2535 2540  
 Leu Cys Val Asn Thr Leu Gly Gly Phe Thr Cys Lys Cys Pro Pro Gly  
 2545 2550 2555 2560  
 Phe Thr Gln His His Thr Ala Cys Ile Asp Asn Asn Glu Cys Gly Ser  
 2565 2570 2575  
 Gln Pro Leu Leu Cys Gly Gly Lys Gly Ile Cys Gln Asn Thr Pro Gly  
 2580 2585 2590  
 Ser Phe Ser Cys Glu Cys Gln Arg Gly Phe Ser Leu Asp Ala Thr Gly  
 2595 2600 2605  
 Leu Asn Cys Glu Asp Val Asp Glu Cys Asp Gly Asn His Arg Cys Gln  
 2610 2615 2620  
 His Gly Cys Gln Asn Ile Leu Gly Gly Tyr Arg Cys Gly Cys Pro Gln  
 2625 2630 2635 2640

Gly Tyr Ile Gln His Tyr Gln Trp Asn Gln Cys Val Asp Glu Asn Glu			
2645	2650	2655	
Cys Ser Asn Pro Asn Ala Cys Gly Ser Ala Ser Cys Tyr Asn Thr Leu			
2660	2665	2670	
Gly Ser Tyr Lys Cys Ala Cys Pro Ser Gly Phe Ser Phe Asp Gln Phe			
2675	2680	2685	
Ser Ser Ala Cys His Asp Val Asn Glu Cys Ser Ser Ser Lys Asn Pro			
2690	2695	2700	
Cys Asn Tyr Gly Cys Ser Asn Thr Glu Gly Gly Tyr Leu Cys Gly Cys			
2705	2710	2715	2720
Pro Pro Gly Tyr Tyr Arg Val Gly Gln Gly His Cys Val Ser Gly Met			
2725	2730	2735	
Gly Phe Asn Lys Gly Gln Tyr Leu Ser Leu Asp Thr Glu Val Asp Glu			
2740	2745	2750	
Glu Asn Ala Leu Ser Pro Glu Ala Cys Tyr Glu Cys Lys Ile Asn Gly			
2755	2760	2765	
Tyr Pro Lys Lys Asp Ser Arg Gln Lys Arg Ser Ile His Glu Pro Asp			
2770	2775	2780	
Pro Thr Ala Val Glu Gln Ile Ser Leu Glu Ser Val Asp Met Asp Ser			
2785	2790	2795	2800
Pro Val Asn Met Lys Phe Asn Leu Ser His Leu Gly Ser Lys Glu His			
2805	2810	2815	
Ile Leu Glu Leu Arg Pro Ala Ile Gln Pro Leu Asn Asn His Ile Arg			
2820	2825	2830	
Tyr Val Ile Ser Gln Gly Asn Asp Asp Ser Val Phe Arg Ile His Gln			
2835	2840	2845	
Arg Asn Gly Leu Ser Tyr Leu His Thr Ala Lys Lys Lys Leu Met Pro			
2850	2855	2860	
Gly Thr Tyr Thr Leu Glu Ile Thr Ser Ile Pro Leu Tyr Lys Lys Lys			
2865	2870	2875	2880
Glu Leu Lys Lys Leu Glu Glu Ser Asn Glu Asp Asp Tyr Leu Leu Gly			
2885	2890	2895	

Glu Leu Gly Glu Ala Leu Arg Met Arg Leu Gln Ile Gln Leu Tyr  
2900 2905 2910

<210> 69  
<211> 2135  
<212> DNA  
<213> Homo sapiens

<400> 69  
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tcccttttcc cagtccactt cgactgctca ggaagtaga gatgtcgctc atcctttaag 120  
tgtatcgagc tgatagctcg atgtgacgga gtctcggatt gcaaagacgg ggaggacgag 180  
taccgctgtg tccgggtggg tggtcagaat gccgtgctcc aggtgttcac agctgcttcg 240  
tggaagacca tgtgtctccg tgactggaag ggtcactacg caaatgttgc ctgtgcccac 300  
ctgggtttcc caagctatgt gagttcagat aacctcagag tgagctcgct ggaggggcag 360  
ttccgggagg agtttgtgtc catcgatcac ctcttgccag atgacaagg gactgcatta 420  
caccactcag tatatgtgag ggagggatgt gcctctggcc acgtggttac cttgcagtgc 480  
acagcctgtg gtcatagaag gggctacagc tcacgcatcg tgggtggaaa catgtccttg 540  
ctctcgagc ggccctggca ggccagcctt cagttccagg gctaccacct gtgcgggggc 600  
tctgtcatca cgcccctgtg gatcatcact gctgcacact gtgtttatga cttgtacctc 660  
cccaagtcac ggaccatcca ggtgggtcta gtttccctgt tggacaatcc agcccatcc 720  
cacttggtgg agaagattgt ctaccacagc aagtacaagc caaagaggct gggcaatgac 780  
atcgccctta tgaagctggc cgggccactc acgttcaatg aaatgatcca gcctgtgtgc 840  
ctgcccact ctgaagagaa cttccccgat ggaaaagtgt gctggacgtc aggatggggg 900  
gccacagagg atggagcagg tgacgcctcc cctgtcctga accacgcggc cgtccctttg 960  
atttccaaca agatctgcaa ccacaggac gtgtacggtg gcatcatctc cccctccatg 1020  
ctctgcgcgg gctacctgac ggggtggcgtg gacagctgcc agggggacag cggggggccc 1080  
ctggtgtgtc aagagaggag gctgtggaag ttagtgggag cgaccagctt tggcatcggc 1140  
tgcgagagg tgaacaagcc tgggggtgtac acccggtgca cctccttctt ggactggatc 1200  
cacgagcaga tggagagaga cctaaaaacc tgaagaggaa ggggacaagt agccacctga 1260  
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ccttccatct gattccagca caaccttcaa gctgcttttt gttttttgtt tttttgaggt 1440  
ggagtctcgc tctgttgccc aggttgaggt gcagtggcga aatccctgct cactgcagcc 1500  
tccgcttccc tggttcaagc gattctcttg cctcagcttc cccagtagct gggaccacag 1560  
gtgcccgcga ccacacccaa ctaatttttg tattttttagt agagacaggg tttcaccatg 1620  
ttggccaggc tgctctcaaa cccctgacct caaatgatgt gcctgcttca gcctcccaca 1680  
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ctctccaggg gtcttgcaaa attcctgacg agataagcag ttatgtgacc tcacgtgcaa 1860  
agccaccaac agccactcag aaaagacgca ccagcccaga agtgcagaac tgcagtcact 1920  
gcacgttttc atctctaggg accagaacca aaccaccctt ttctacttcc aagacttatt 1980  
ttcacatgtg gggaggttaa tctaggaatg actcgtttaa ggccatattt catgatttct 2040  
ttgtagcatt tgggtgcttg cgtattattg tccttttgatt ccaaataata tgtttccttc 2100  
cctcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2135



<210> 70  
 <211> 790  
 <212> PRT  
 <213> Sus scrofa

<400> 70  
 Asp Ser Leu Asp Asp Tyr Val Asn Thr Gln Gly Ala Phe Leu Phe Ser  
 1 5 10 15  
 Leu Ser Arg Lys Gln Val Ala Ala Arg Ser Val Glu Glu Cys Ala Ala  
 20 25 30  
 Lys Cys Glu Ala Glu Thr Asn Phe Ile Cys Arg Ala Phe Gln Tyr His  
 35 40 45  
 Ser Lys Asp Gln Gln Cys Val Val Met Ala Glu Asn Ser Lys Thr Ser  
 50 55 60  
 Pro Ile Ala Arg Met Arg Asp Val Val Leu Phe Glu Lys Arg Ile Tyr  
 65 70 75 80  
 Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly Thr Thr  
 85 90 95  
 Ser Lys Thr Lys Ser Gly Val Ile Cys Gln Lys Trp Ser Val Ser Ser  
 100 105 110  
 Pro His Ile Pro Lys Tyr Ser Pro Glu Lys Phe Pro Leu Ala Gly Leu  
 115 120 125  
 Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Lys Gly Pro Trp  
 130 135 140  
 Cys Tyr Thr Thr Asp Pro Glu Thr Arg Phe Asp Tyr Cys Asp Ile Pro  
 145 150 155 160  
 Glu Cys Glu Asp Glu Cys Met His Cys Ser Gly Glu His Tyr Glu Gly  
 165 170 175  
 Lys Ile Ser Lys Thr Met Ser Gly Ile Glu Cys Gln Ser Trp Gly Ser  
 180 185 190  
 Gln Ser Pro His Ala His Gly Tyr Leu Pro Ser Lys Phe Pro Asn Lys  
 195 200 205  
 Asn Leu Lys Met Asn Tyr Cys Arg Asn Pro Asp Gly Glu Pro Arg Pro  
 210 215 220

Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Phe Cys Asp Ile			
225	230	235	240
Pro Arg Cys Thr Thr Pro Pro Pro Thr Ser Gly Pro Thr Tyr Gln Cys			
	245	250	255
Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser Val Thr Ala			
	260	265	270
Ser Gly His Thr Cys Gln Arg Trp Ser Ala Gln Ser Pro His Lys His			
	275	280	285
Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Glu Glu Asn Tyr			
	290	295	300
Cys Arg Asn Pro Asp Gly Glu Thr Ala Pro Trp Cys Tyr Thr Thr Asp			
305	310	315	320
Ser Glu Val Arg Trp Asp Tyr Cys Lys Ile Pro Ser Cys Gly Ser Ser			
	325	330	335
Thr Thr Ser Thr Glu His Leu Asp Ala Pro Val Pro Pro Glu Gln Thr			
	340	345	350
Pro Val Ala Gln Asp Cys Tyr Arg Gly Asn Gly Glu Ser Tyr Arg Gly			
	355	360	365
Thr Ser Ser Thr Thr Ile Thr Gly Arg Lys Cys Gln Ser Trp Val Ser			
	370	375	380
Met Thr Pro His Arg His Glu Lys Thr Pro Gly Asn Phe Pro Asn Ala			
385	390	395	400
Gly Leu Thr Met Asn Tyr Cys Arg Asn Pro Asp Ala Asp Lys Ser Pro			
	405	410	415
Trp Cys Tyr Thr Thr Asp Pro Arg Val Arg Trp Glu Tyr Cys Asn Leu			
	420	425	430
Lys Lys Cys Ser Glu Thr Glu Gln Gln Val Thr Asn Phe Pro Ala Ile			
	435	440	445
Ala Gln Val Pro Ser Val Glu Asp Leu Ser Glu Asp Cys Met Phe Gly			
	450	455	460
Asn Gly Lys Arg Tyr Arg Gly Lys Arg Ala Thr Thr Val Ala Gly Val			
465	470	475	480

Pro	Cys	Gln	Glu	Trp	Ala	Ala	Gln	Glu	Pro	His	Arg	His	Ser	Ile	Phe	485	490	495	
Thr	Pro	Glu	Thr	Asn	Pro	Arg	Ala	Gly	Leu	Glu	Lys	Asn	Tyr	Cys	Arg	500	505	510	
Asn	Pro	Asp	Gly	Asp	Asp	Asn	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asn	Pro	515	520	525	
Gln	Lys	Leu	Phe	Asp	Tyr	Cys	Asp	Val	Pro	Gln	Cys	Val	Thr	Ser	Ser	530	535	540	
Phe	Asp	Cys	Gly	Lys	Pro	Lys	Val	Glu	Pro	Lys	Lys	Cys	Pro	Ala	Arg	545	550	555	560
Val	Val	Gly	Gly	Cys	Val	Ser	Ile	Pro	His	Ser	Trp	Pro	Trp	Gln	Ile	565	570	575	
Ser	Leu	Arg	Tyr	Arg	Tyr	Arg	Gly	His	Phe	Cys	Gly	Gly	Thr	Leu	Ile	580	585	590	
Ser	Pro	Glu	Trp	Val	Leu	Thr	Ala	Lys	His	Cys	Leu	Glu	Lys	Ser	Ser	595	600	605	
Ser	Pro	Ser	Ser	Tyr	Lys	Val	Ile	Leu	Gly	Ala	His	Glu	Glu	Tyr	His	610	615	620	
Leu	Gly	Glu	Gly	Val	Gln	Glu	Ile	Asp	Val	Ser	Lys	Leu	Phe	Lys	Glu	625	630	635	640
Pro	Ser	Glu	Ala	Asp	Ile	Ala	Leu	Leu	Lys	Leu	Ser	Ser	Pro	Ala	Val	645	650	655	
Ile	Thr	Asp	Lys	Val	Ile	Pro	Ala	Cys	Leu	Pro	Thr	Pro	Asn	Tyr	Val	660	665	670	
Val	Ala	Asp	Arg	Thr	Ala	Cys	Tyr	Ile	Thr	Gly	Trp	Gly	Glu	Thr	Lys	675	680	685	
Gly	Thr	Tyr	Gly	Ala	Gly	Leu	Leu	Lys	Glu	Ala	Arg	Leu	Pro	Val	Ile	690	695	700	
Glu	Asn	Lys	Val	Cys	Asn	Arg	Tyr	Glu	Tyr	Leu	Gly	Gly	Lys	Val	Ser	705	710	715	720
Pro	Asn	Glu	Leu	Cys	Ala	Gly	His	Leu	Ala	Gly	Gly	Ile	Asp	Ser	Cys	725	730	735	

Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr  
740 745 750

Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Leu Pro Asn  
755 760 765

Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu  
770 775 780

Glu Ile Met Arg Arg Asn  
785 790

<210> 71  
<211> 812  
<212> PRT  
<213> Bos taurus

<400> 71  
Met Leu Pro Ala Ser Pro Lys Met Glu His Lys Ala Val Val Phe Leu  
1 5 10 15

Leu Leu Leu Phe Leu Lys Ser Gly Leu Gly Asp Leu Leu Asp Asp Tyr  
20 25 30

Val Asn Thr Gln Gly Ala Ser Leu Leu Ser Leu Ser Arg Lys Asn Leu  
35 40 45

Ala Gly Arg Ser Val Glu Asp Cys Ala Ala Lys Cys Glu Glu Glu Thr  
50 55 60

Asp Phe Val Cys Arg Ala Phe Gln Tyr His Ser Lys Glu Gln Gln Cys  
65 70 75 80

Val Val Met Ala Glu Asn Ser Lys Asn Thr Pro Val Phe Arg Met Arg  
85 90 95

Asp Val Ile Leu Tyr Glu Lys Arg Ile Tyr Leu Leu Glu Cys Lys Thr  
100 105 110

Gly Asn Gly Gln Thr Tyr Arg Gly Thr Thr Ala Glu Thr Lys Ser Gly  
115 120 125

Val Thr Cys Gln Lys Trp Ser Ala Thr Ser Pro His Val Pro Lys Phe  
130 135 140

Ser Pro Glu Lys Phe Pro Leu Ala Gly Leu Glu Glu Asn Tyr Cys Arg

145		150		155		160
Asn Pro Asp Asn Asp Glu Asn Gly Pro Trp Cys Tyr Thr Thr Asp Pro						
	165		170		175	
Asp Lys Arg Tyr Asp Tyr Cys Asp Ile Pro Glu Cys Glu Asp Lys Cys						
	180		185		190	
Met His Cys Ser Gly Glu Asn Tyr Glu Gly Lys Ile Ala Lys Thr Met						
	195		200		205	
Ser Gly Arg Asp Cys Gln Ala Trp Asp Ser Gln Ser Pro His Ala His						
	210		215		220	
Gly Tyr Ile Pro Ser Lys Phe Pro Asn Lys Asn Leu Lys Met Asn Tyr						
	225		230		235	240
Cys Arg Asn Pro Asp Gly Glu Pro Arg Pro Trp Cys Phe Thr Thr Asp						
	245		250		255	
Pro Gln Lys Arg Trp Glu Phe Cys Asp Ile Pro Arg Cys Thr Thr Pro						
	260		265		270	
Pro Pro Ser Ser Gly Pro Lys Tyr Gln Cys Leu Lys Gly Thr Gly Lys						
	275		280		285	
Asn Tyr Gly Gly Thr Val Ala Val Thr Glu Ser Gly His Thr Cys Gln						
	290		295		300	
Arg Trp Ser Glu Gln Thr Pro His Lys His Asn Arg Thr Pro Glu Asn						
	305		310		315	320
Phe Pro Cys Lys Asn Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asn Gly						
	325		330		335	
Glu Lys Ala Pro Trp Cys Tyr Thr Thr Asn Ser Glu Val Arg Trp Glu						
	340		345		350	
Tyr Cys Thr Ile Pro Ser Cys Glu Ser Ser Pro Leu Ser Thr Glu Arg						
	355		360		365	
Met Asp Val Pro Val Pro Pro Glu Gln Thr Pro Val Pro Gln Asp Cys						
	370		375		380	
Tyr His Gly Asn Gly Gln Ser Tyr Arg Gly Thr Ser Ser Thr Thr Ile						
	385		390		395	400
Thr Gly Arg Lys Cys Gln Ser Trp Ser Ser Met Thr Pro His Arg His						

405	410	415
Leu Lys Thr Pro Glu Asn Tyr	Pro Asn Ala Gly Leu Thr	Met Asn Tyr
420	425	430
Cys Arg Asn Pro Asp Ala Asp	Lys Ser Pro Trp Cys Tyr Thr Thr	Asp
435	440	445
Pro Arg Val Arg Trp Glu Phe Cys Asn Leu Lys Lys Cys Ser Glu Thr		
450	455	460
Pro Glu Gln Val Pro Ala Ala Pro Gln Ala Pro Gly Val Glu Asn Pro		
465	470	475
Pro Glu Ala Asp Cys Met Ile Gly Thr Gly Lys Ser Tyr Arg Gly Lys		
485	490	495
Lys Ala Thr Thr Val Ala Gly Val Pro Cys Gln Glu Trp Ala Ala Gln		
500	505	510
Glu Pro His Gln His Ser Ile Phe Thr Pro Glu Thr Asn Pro Gln Ser		
515	520	525
Gly Leu Glu Arg Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Asn Gly		
530	535	540
Pro Trp Cys Tyr Thr Met Asn Pro Arg Lys Pro Phe Asp Tyr Cys Asp		
545	550	555
Val Pro Gln Cys Glu Ser Ser Phe Asp Cys Gly Lys Pro Lys Val Glu		
565	570	575
Pro Lys Lys Cys Ser Gly Arg Ile Val Gly Gly Cys Val Ser Lys Pro		
580	585	590
His Ser Trp Pro Trp Gln Val Ser Leu Arg Arg Ser Ser Arg His Phe		
595	600	605
Cys Gly Gly Thr Leu Ile Ser Pro Lys Trp Val Leu Thr Ala Ala His		
610	615	620
Cys Leu Asp Asn Ile Leu Ala Leu Ser Phe Tyr Lys Val Ile Leu Gly		
625	630	635
Ala His Asn Glu Lys Val Arg Glu Gln Ser Val Gln Glu Ile Pro Val		
645	650	655
Ser Arg Leu Phe Arg Glu Pro Ser Gln Ala Asp Ile Ala Leu Leu Lys		

660	665	670
Leu Ser Arg Pro Ala Ile Ile Thr Lys Glu Val Ile Pro Ala Cys Leu		
675	680	685
Pro Pro Pro Asn Tyr Met Val Ala Ala Arg Thr Glu Cys Tyr Ile Thr		
690	695	700
Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Glu Gly Leu Leu Lys Glu		
705	710	715
Ala His Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Asn Glu Tyr		
725	730	735
Leu Asp Gly Arg Val Lys Pro Thr Glu Leu Cys Ala Gly His Leu Ile		
740	745	750
Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys		
755	760	765
Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu		
770	775	780
Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Pro		
785	790	795
Tyr Val Pro Trp Ile Glu Glu Thr Met Arg Arg Asn		
805	810	

<210> 72  
 <211> 229  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Consensus  
 Sequence

<400> 72  
 Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln  
 1 5 10 15  
 Val Ser Leu Gln Tyr Arg Gly Gly Gly Arg His Phe Cys Gly Gly Ser  
 20 25 30  
 Leu Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly  
 35 40 45

Ser Asp Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser  
 50 55 60  
 Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro  
 65 70 75 80  
 Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu  
 85 90 95  
 Lys Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro  
 100 105 110  
 Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly  
 115 120 125  
 Trp Gly Arg Thr Ser Glu Ser Gly Gly Ser Leu Pro Asp Thr Leu Gln  
 130 135 140  
 Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr  
 145 150 155 160  
 Ser Gly Gly Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu Glu  
 165 170 175  
 Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
 180 185 190  
 Asn Asp Asn Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser Asp  
 195 200 205  
 Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser  
 210 215 220  
 Tyr Leu Asp Trp Ile  
 225

<210> 73  
 <211> 2646  
 <212> DNA  
 <213> Homo sapiens

<400> 73  
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 atttgaataa aacagcagag tcagcatctt cagagaaaaa gaaaacaaga cgctgcaatg 120  
 gattcaagat gttcttggca gccctgtcat tcagctatat tgctaaagca ctaggtggaa 180  
 tcattatgaa aatttccatc actcaaatag aaaggagatt tgacatatcc tcttctcttg 240



ctggtttaat tgatggaagc tttgaaattg gaaatttgct tgtgattgta tttgtaagtt 300  
 actttggatc taaactacac agaccgaagt taattggaat tggttgtctc cttatgggaa 360  
 ctggaagtat tttgacatct ttaccacatt tcttcatggg atattatagg tattctaaag 420  
 aaacccatat taatccatca gaaaattcaa catcaagttt atcaacctgt ttaattaatc 480  
 aaaccttatc attcaatgga acatcacctg agatagtaga aaaagattgt gtaaaggaat 540  
 ctgggtcaca catgtggatc tatgtcttca tggggaatat gcttcgtggc ataggggaaa 600  
 ccccatagat accattgggg atttcataca ttgatgattt tgcaaaagaa ggacattctt 660  
 ccttgatattt aggtagtttg aatgcaatag gaatgattgg tccagtcatt ggctttgcac 720  
 tgggatctct gtttgctaaa atgtacgtgg atattggata tgtagatctg agcactatca 780  
 gaataactcc taaggactct cgttgggttg gagcttgggt gcttggtttc cttgtgtctg 840  
 gactattttc cattattttc tccataccat tttttttctt gccgaaaaat ccaaataaac 900  
 cacaaaaaga aagaaaaatt tcactatcat tgcattgtgt gaaaacaaat gatgatagaa 960  
 atcaaacagc taatttgacc aaccaaggaa aaaatgttac caaaaatgtg actgggtttt 1020  
 tccagtcttt gaaaagcatc cttaccaatc ccctgtatgt tatattttctg cttttgacat 1080  
 tgttacaagt aagcagcttt attggttctt ttacttacgt ctttaaatat atggagcaac 1140  
 agtacgggtc gtctgcatct catgctaact tttgttggg aatcataacc attcctacgg 1200  
 ttgcaactgg aatgttttta ggaggattta tcattaaaaa attcaaattg tctttagttg 1260  
 gaattgccaa attttcattt cttacttcga tgatatactt cttgtttcaa cttctatatt 1320  
 tccctctaatt ctgcgaaagc aaatcagttg ccggcctaac cttgacctat gatggaaata 1380  
 attcagtggc atctcatgta gatgtaccac tttcttattg caactcagag tgcaattgtg 1440  
 atgaaagtca gtgggaacca gtctgtggga acaatggaat aacttacctg tcacctgtc 1500  
 tagcaggatg caaatcctca agtggtatta aaaagcatc agtgttttat aactgtagtt 1560  
 gtgtggaagt aactgggtct cagaacagaa attactcagc acacttgggt gaatgcccaa 1620  
 gagataatac ttgtacaagg aaatttttca tctatgttgc aattcaagtc ataaactctt 1680  
 tgttctctgc aacaggaggt accacattta tcttgttgac tgtgaagatt gttcaacctg 1740  
 aattgaaagc acttgcaatg ggtttccagt caatggttat aagaacacta ggaggaattc 1800  
 tagctccaat atattttggg gctctgattg ataaaacatg tatgaagtgg tccaccaaca 1860  
 gctgtggagc acaaggagct tgtaggatat ataattccgt attttttgga agggctctact 1920  
 tgggcttata tatagcttta agattcccag cacttgtttt atatattgtt ttcatttttg 1980  
 ctatgaagaa aaaatttcaa ggaaaagata ccaaggcatc ggacaatgaa agaaaagtaa 2040  
 tggatgaagc aaacttagaa ttcttaataa atggtgaaca ttttgtacct tctgctggaa 2100  
 cagatagtaa aacatgtaat ttggacatgc aagacaatgc tgctgccaac taacattgca 2160  
 ttgattcatt aagatgttat ttttgagggt ttcttgggtc ttactgaca attccaacat 2220  
 tctttactta cagtggacca atggataagt ctatgcatct ataataaact ataaaaaatg 2280  
 ggagtaccca tggtaggat atagctatgc ctttatgggt aagattagaa tatatgatcc 2340  
 ataaaattta aagtgaagg catggttagt gtgtgatata ataaaaagta attgtttgggt 2400  
 agttgtaact gctaataaaa ccagtgacta gaataaagg gaggtaaaaa ggacaagata 2460  
 gattaatagc ctaataaaag agaaaagcct gatgccttta aaaaatgaaa cactttggat 2520  
 gtattactta ggccaaaatc tggcctggat ttatgctata atatataatt tcatgttaag 2580  
 ttgtatatatt ttcagaaatt ataaatatta ttaatttaaa attcgaaaaa aaaaaaaaaa 2640  
 aaaaaa 2646

<210> 74  
 <211> 691  
 <212> PRT  
 <213> Homo sapiens

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<400> 74
Met Asp Gln Asn Gln His Leu Asn Lys Thr Ala Glu Ala Gln Pro Ser
 1              5              10              15

Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys Met Phe Leu Ala
      20              25              30

Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
      35              40              45

Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
      50              55              60

Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
      65              70              75              80

Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
      85              90              95

Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
      100             105             110

Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser Lys Glu Thr Asn
      115             120             125

Ile Asn Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
      130             135             140

Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
      145             150             155             160

Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met
      165             170             175

Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
      180             185             190

Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr
      195             200             205

Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro Ile Ile Gly Phe
      210             215             220

Thr Leu Gly Ser Leu Phe Ser Lys Met Tyr Val Asp Ile Gly Tyr Val
      225             230             235             240

Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser Arg Trp Val Gly
      245             250             255

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Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser	260	265	270
Ser Ile Pro Phe Phe Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys	275	280	285
Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu	290	295	300
Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys	305	310	315
Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro	325	330	335
Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr	340	345	350
Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu Gln Gln Tyr Gly	355	360	365
Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro	370	375	380
Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile Ile Lys Lys Phe	385	390	395
Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys Phe Thr Ala Val	405	410	415
Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn	420	425	430
Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val	435	440	445
Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn	450	455	460
Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr	465	470	475
Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys	485	490	495
Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu	500	505	510

Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp  
515 520 525

Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn  
530 535 540

Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val Met Leu Ile Val  
545 550 555 560

Lys Ile Val Gln Pro Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser  
565 570 575

Met Val Ile Arg Ala Leu Gly Gly Ile Leu Ala Pro Ile Tyr Phe Gly  
580 585 590

Ala Leu Ile Asp Thr Thr Cys Ile Lys Trp Ser Thr Asn Asn Cys Gly  
595 600 605

Thr Arg Gly Ser Cys Arg Thr Tyr Asn Ser Thr Ser Phe Ser Arg Val  
610 615 620

Tyr Leu Gly Leu Ser Ser Met Leu Arg Val Ser Ser Leu Val Leu Tyr  
625 630 635 640

Ile Ile Leu Ile Tyr Ala Met Lys Lys Lys Tyr Gln Glu Lys Asp Ile  
645 650 655

Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala Asn Leu Glu Ser  
660 665 670

Leu Asn Lys Asn Lys His Phe Val Pro Ser Ala Gly Ala Asp Ser Glu  
675 680 685

Thr His Cys  
690

<210> 75

<211> 204

<212> DNA

<213> Rattus norvegicus

<400> 75

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tggggggact tgcttcccg gccaggacgg ctgtgactgc ccagagggct ggactggaat 180  
catctgcaat gagactgtc ctcc 204

<210> 76  
 <211> 91  
 <212> DNA  
 <213> Rattus norvegicus

<400> 76  
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 gggatgagct gcccgcactc ttccaggatg a 91

<210> 77  
 <211> 1574  
 <212> PRT  
 <213> Rattus norvegicus

<400> 77  
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 Pro Arg Pro Leu Gln Pro Ser Met Pro His Val Cys Ala Glu Gln Lys  
 35 40 45  
 Leu Thr Leu Val Gly His Arg Gln Pro Cys Val Gln Ala Phe Ser Arg  
 50 55 60  
 Ile Val Pro Val Trp Arg Arg Thr Gly Cys Ala Gln Gln Ala Trp Cys  
 65 70 75 80  
 Ile Gly Gln Glu Arg Arg Thr Val Tyr Tyr Met Ser Tyr Arg Gln Val  
 85 90 95  
 Tyr Ala Thr Glu Ala Arg Thr Val Phe Arg Cys Cys Pro Gly Trp Ser  
 100 105 110  
 Gln Lys Pro Gly Gln Glu Gly Cys Leu Ser Asp Val Asp Glu Cys Ala  
 115 120 125  
 Ser Ala Asn Gly Gly Cys Glu Gly Pro Cys Cys Asn Thr Val Gly Gly  
 130 135 140  
 Phe Tyr Cys Arg Cys Pro Pro Gly Tyr Gln Leu Gln Gly Asp Gly Lys  
 145 150 155 160

Thr Cys Gln Asp Val Asp Glu Cys Arg Ala His Asn Gly Gly Cys Gln	165	170	175
His Arg Cys Val Asn Thr Pro Gly Ser Tyr Leu Cys Glu Cys Lys Pro	180	185	190
Gly Phe Arg Leu His Thr Asp Gly Arg Thr Cys Leu Ala Ile Ser Ser	195	200	205
Cys Thr Leu Gly Asn Gly Gly Cys Gln His Gln Cys Val Gln Leu Thr	210	215	220
Val Thr Gln His Arg Cys Gln Cys Arg Pro Gln Tyr Gln Leu Gln Glu	225	230	235
Asp Gly Arg Arg Cys Val Arg Arg Ser Pro Cys Ala Glu Gly Asn Gly	245	250	255
Gly Cys Met His Ile Cys Gln Glu Leu Arg Gly Leu Ala His Cys Gly	260	265	270
Cys His Pro Gly Tyr Gln Leu Ala Ala Asp Arg Lys Thr Cys Glu Asp	275	280	285
Val Asp Glu Cys Ala Leu Gly Leu Ala Gln Cys Ala His Gly Cys Leu	290	295	300
Asn Thr Gln Gly Ser Phe Lys Cys Val Cys His Ala Gly Tyr Glu Leu	305	310	315
Gly Ala Asp Gly Arg Gln Cys Tyr Arg Ile Glu Met Glu Ile Val Asn	325	330	335
Ser Cys Glu Ala Gly Asn Gly Gly Cys Ser His Gly Cys Ser His Thr	340	345	350
Ser Thr Gly Pro Leu Cys Thr Cys Pro Arg Gly Tyr Glu Leu Asp Glu	355	360	365
Asp Gln Lys Thr Cys Ile Asp Ile Asp Asp Cys Ala Asn Ser Pro Cys	370	375	380
Cys Gln Gln Ala Cys Ala Asn Thr Pro Gly Gly Tyr Glu Cys Ser Cys	385	390	395
Phe Ala Gly Tyr Arg Leu Asn Thr Asp Gly Cys Gly Cys Glu Asp Val	405	410	415

Asp Glu Cys Ala Ser Gly His Gly Gly Cys Glu His His Cys Ser Asn  
 420 425 430

Leu Ala Gly Ser Phe Gln Cys Phe Cys Glu Ala Gly Tyr Arg Leu Asp  
 435 440 445

Glu Asp Arg Arg Gly Cys Thr Ser Leu Glu Glu Ser Val Val Asp Leu  
 450 455 460

Asp Gly Arg Leu Pro Phe Val Arg Pro Leu Pro His Ile Ala Val Leu  
 465 470 475 480

Arg Asp Glu Leu Pro Arg Leu Phe Gln Asp Asp Tyr Gly Ala Glu Glu  
 485 490 495

Glu Ala Ala Ala Ala Glu Leu Arg Gly Glu His Thr Leu Thr Glu Lys  
 500 505 510

Phe Val Cys Leu Asp His Ser Phe Gly His Asp Cys Ser Leu Thr Cys  
 515 520 525

Asp Asp Cys Arg Asn Gly Gly Thr Cys Phe Pro Gly Gln Asp Gly Cys  
 530 535 540

Asp Cys Pro Glu Gly Trp Thr Gly Ile Ile Cys Asn Glu Thr Cys Pro  
 545 550 555 560

Pro Asp Thr Phe Gly Lys Asn Cys Ser Ser Pro Cys Thr Cys Gln Asn  
 565 570 575

Gly Gly Thr Cys Asp Pro Val Leu Gly Ala Cys Arg Cys Pro Pro Gly  
 580 585 590

Val Ser Gly Ala His Cys Glu Asp Gly Cys Pro Lys Gly Phe Tyr Gly  
 595 600 605

Lys His Cys Arg Lys Lys Cys His Cys Ala Asn Arg Gly Arg Cys His  
 610 615 620

Arg Leu Tyr Gly Ala Cys Leu Cys Asp Pro Gly Leu Tyr Gly Arg Phe  
 625 630 635 640

Cys His Leu Ala Cys Pro Pro Trp Ala Phe Gly Pro Gly Cys Ser Glu  
 645 650 655

Asp Cys Leu Cys Glu Gln Ser His Thr Arg Ser Cys Asn Pro Lys Asp  
 660 665 670

Gly Ser Cys Ser Cys Lys Ala Gly Phe Gln Gly Glu Arg Cys Gln Ala  
 675 680 685

Glu Cys Glu Ser Gly Phe Phe Gly Pro Gly Cys Arg His Arg Cys Thr  
 690 695 700

Cys Gln Pro Gly Val Ala Cys Asp Pro Val Ser Gly Glu Cys Arg Thr  
 705 710 715 720

Gln Cys Pro Pro Gly Tyr Gln Gly Glu Asp Cys Gly Gln Glu Cys Pro  
 725 730 735

Val Gly Thr Phe Gly Val Asn Cys Ser Gly Ser Cys Ser Cys Val Gly  
 740 745 750

Ala Pro Cys His Arg Val Thr Gly Glu Cys Leu Cys Pro Pro Gly Lys  
 755 760 765

Thr Gly Glu Asp Cys Gly Ala Asp Cys Pro Glu Gly Arg Trp Gly Leu  
 770 775 780

Gly Cys Gln Glu Ile Cys Pro Ala Cys Glu His Gly Ala Ser Cys Asn  
 785 790 795 800

Pro Glu Thr Gly Thr Cys Leu Cys Leu Pro Gly Phe Val Gly Ser Arg  
 805 810 815

Cys Gln Asp Thr Cys Ser Ala Gly Trp Tyr Gly Thr Gly Cys Gln Ile  
 820 825 830

Arg Cys Ala Cys Ala Asn Asp Gly His Cys Asp Pro Thr Thr Gly Arg  
 835 840 845

Cys Ser Cys Ala Pro Gly Trp Thr Gly Leu Ser Cys Gln Arg Ala Cys  
 850 855 860

Asp Ser Gly His Trp Gly Pro Asp Cys Ile His Pro Cys Asn Cys Ser  
 865 870 875 880

Ala Gly His Gly Asn Cys Asp Ala Val Ser Gly Leu Cys Leu Cys Glu  
 885 890 895

Ala Gly Tyr Glu Gly Pro Arg Cys Glu Gln Ser Cys Arg Gln Gly Tyr  
 900 905 910

Tyr Gly Pro Ser Cys Glu Gln Lys Cys Arg Cys Glu His Gly Ala Ala  
 915 920 925



Cys Asp His Val Ser Gly Ala Cys Thr Cys Pro Ala Gly Trp Arg Gly  
 930 935 940

Ser Phe Cys Glu His Ala Cys Pro Ala Gly Phe Phe Gly Leu Asp Cys  
 945 950 955 960

Asp Ser Ala Cys Asn Cys Ser Ala Gly Ala Pro Cys Asp Ala Val Thr  
 965 970 975

Gly Ser Cys Ile Cys Pro Ala Gly Arg Trp Gly Pro Arg Cys Ala Gln  
 980 985 990

Ser Cys Pro Pro Leu Thr Phe Gly Leu Asn Cys Ser Gln Ile Cys Thr  
 995 1000 1005

Cys Phe Asn Gly Ala Ser Cys Asp Ser Val Thr Gly Gln Cys His Cys  
 1010 1015 1020

Ala Pro Gly Trp Met Gly Pro Thr Cys Leu Gln Ala Cys Pro Pro Gly  
 1025 1030 1035 1040

Leu Tyr Gly Lys Asn Cys Gln His Ser Cys Leu Cys Arg Asn Gly Gly  
 1045 1050 1055

Arg Cys Asp Pro Ile Leu Gly Gln Cys Thr Cys Pro Glu Gly Trp Thr  
 1060 1065 1070

Gly Leu Ala Cys Glu Asn Glu Cys Leu Pro Gly His Tyr Ala Ala Gly  
 1075 1080 1085

Cys Gln Leu Asn Cys Ser Cys Leu His Gly Gly Ile Cys Asp Arg Leu  
 1090 1095 1100

Thr Gly His Cys Leu Cys Pro Ala Gly Trp Thr Gly Asp Lys Cys Gln  
 1105 1110 1115 1120

Ser Ser Cys Val Ser Gly Thr Phe Gly Val His Cys Glu Glu His Cys  
 1125 1130 1135

Ala Cys Arg Lys Gly Ala Ser Cys His His Val Thr Gly Ala Cys Phe  
 1140 1145 1150

Cys Pro Pro Gly Trp Arg Gly Pro His Cys Glu Gln Ala Cys Pro Arg  
 1155 1160 1165

Gly Trp Phe Gly Glu Ala Cys Ala Gln Arg Cys Leu Cys Pro Thr Asn  
 1170 1175 1180

Ala Ser Cys His His Val Thr Gly Glu Cys Arg Cys Pro Pro Gly Phe			
1185	1190	1195	1200
Thr Gly Leu Ser Cys Glu Gln Ala Cys Gln Pro Gly Thr Phe Gly Lys			
	1205	1210	1215
Asp Cys Glu His Leu Cys Gln Cys Pro Gly Glu Thr Trp Ala Cys Asp			
	1220	1225	1230
Pro Ala Ser Gly Val Cys Thr Cys Ala Ala Gly Tyr His Gly Thr Gly			
	1235	1240	1245
Cys Leu Gln Arg Cys Pro Ser Gly Arg Tyr Gly Pro Gly Cys Glu His			
	1250	1255	1260
Ile Cys Lys Cys Leu Asn Gly Gly Thr Cys Asp Pro Ala Thr Gly Ala			
1265	1270	1275	1280
Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp Cys Ser Leu Ala Cys			
	1285	1290	1295
Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His Val Cys Ala Cys Arg			
	1300	1305	1310
Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Ala Cys Ile Cys Ser Pro			
	1315	1320	1325
Gly Lys Thr Gly Val Arg Cys Glu His Gly Cys Pro Gln Asp Arg Phe			
	1330	1335	1340
Gly Lys Gly Cys Glu Leu Lys Cys Ala Cys Arg Asn Gly Gly Leu Cys			
1345	1350	1355	1360
His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu Gly Trp Met Gly Pro			
	1365	1370	1375
His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr Gly Ala Ala Cys Leu			
	1380	1385	1390
Leu Glu Cys Phe Cys Gln Asn Asn Gly Ser Cys Glu Pro Thr Thr Gly			
	1395	1400	1405
Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln Ala Cys Glu His Ser			
	1410	1415	1420
Cys Pro Ser Gly Phe His Gly Pro Gly Cys Gln Arg Val Cys Glu Cys			
1425	1430	1435	1440

Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly Gln Cys Leu Cys Pro  
1445 1450 1455

Ala Gly Phe His Gly Gln Phe Cys Glu Lys Gly Cys Glu Ser Gly Ser  
1460 1465 1470

Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys His Thr Gly Val Pro  
1475 1480 1485

Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro Pro Gly Arg Thr Gly  
1490 1495 1500

Ala Ala Cys Asp Leu Asp Cys Arg Arg Gly Arg Phe Gly Pro Gly Cys  
1505 1510 1515 1520

Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp Cys Asp Pro Ile Ser  
1525 1530 1535

Gly Gln Cys His Cys Val Asp Ser Tyr Met Gly Pro Thr Cys Arg Glu  
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Val Pro Thr Gln Ile Ser Ser Ser Arg Pro Ala Pro Gln His Pro Ser  
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Ser Arg Ala Met Lys His  
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<210> 78  
<211> 1708  
<212> DNA  
<213> Homo sapiens

<400> 78  
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cgccggtgcg tccccaggc tggtagccga gctgcagggc gccctggacg cctgcgcaca 180  
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aatggcccca tccgctgctc ctcaggcccc agaagccttc acactcaagg agaaggggca 720  
cctgctgcgg ctgcctgcgg cattcaggaa agcagcttcc cagaactcga gcctgtgggc 780  
ccagctcagt tccacacaga ccagtgattc cacggatgcc gccgctgccca aaaccagtt 840

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ggaggcggag gcggggcgcc tgcggaaggc ctgctcgctg ctgagactgc gcatgagggg 960
ggagctctca gcagccccc tggactggat gcaggagtac cgctgcctgc tcacgctgga 1020
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ggcggaacag ccaccaagac catgtcctgt ggggaggccc cccggagcct cgccgtcctg 1140
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gccctggctg gccctgtgcc gggctgtgca cagcctgctc tgcgaggagg gagcacgtgt 1380
ccttaccatc ctgcgggatg aacctgcagt ctgagccttt cccatgctgc cctcggcctg 1440
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gtgtgatatt aaagccactt tagaaagc 1708

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<210> 79

<211> 1151

<212> PRT

<213> Gallus gallus

<400> 79

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Arg Ser Pro Thr Pro Pro Pro Arg Asn Pro Pro Thr Pro Pro Pro Ala
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Pro Ser Pro Ala Pro Ala Pro Ala Pro Ala Pro Thr Ala Pro Pro Arg
20 25 30

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Pro Lys Trp Val Pro Ile Ala Glu Leu His Pro Ala Ala Pro Gln Pro
35 40 45

```

```

Pro Pro Lys Trp Val Pro Ile Gly Gly Ala Pro Pro Pro Pro Gly Thr
50 55 60

```

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Glu Pro Thr Pro Pro Ser Lys Pro Thr Asp Gly Ala Asp Ala Ala Pro
65 70 75 80

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```

Lys Ala Ser Ala Glu Leu Thr Ser Pro Pro Pro Ala Ser Pro Ser Pro
85 90 95

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Pro Asp Gly Pro Lys Ala Pro Ser Gly Ala Gly Glu Ala Glu Ala Gly
100 105 110

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Thr Pro Pro Pro Ser Gln Gly Pro Ala Gly Thr Pro Pro Pro Ser Gln
115 120 125

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Gly Ala Ala Gly Ala Pro Lys Gly Asp Gly Thr Ala Gln Pro Ser Gly

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130		135		140	
Thr Lys Ser Gly Ala Asp Gly Lys Pro Ala Ala Gln Asp Val Pro Lys					
145		150		155	160
Ala Thr Thr Ala Ala Thr Glu Ala Arg Pro Ala Ser Ala Ala Ser Pro					
	165		170		175
Thr Val Pro Lys Ala Thr Ala Glu Ala Thr Ala Val Thr Ala Ala Ser					
	180		185		190
Gln Ser Ala Pro Lys Ala Ala Thr Asp Ala Ala Ala Val Thr Ala Ala					
	195		200		205
Ser Gln Ser Ala Pro Lys Ala Thr Val Glu Val Lys Pro Ala Ala Ala					
	210		215		220
Ala Val Ala Lys Glu Ala Lys Ala Val Thr Ala Ala Ala Ala Ala Pro					
225		230		235	240
Lys Ala Thr Ala Glu Ala Lys Pro Ala Pro Val Thr Ser Pro Thr Ile					
	245		250		255
Pro Cys Ser Ser Ala Glu Ala Lys Pro Leu Thr Ala Ala Ser Pro Thr					
	260		265		270
Ala Ser Lys Ala Thr Ala Glu Ala Lys Pro Val Pro Ala Thr Ala Ser					
	275		280		285
Leu Met Ala Thr Lys Val Thr Ala Glu Ala Lys Pro Ala Pro Ser Pro					
	290		295		300
Ser Val Pro Lys Ala Thr Thr Asp Thr Lys Ala Val Thr Ala Thr Ala					
305		310		315	320
Pro Lys Ala Gly Pro Asp Val Lys Pro Ala Val Ala Val Cys Ala Glu					
	325		330		335
Ala Lys Pro Ala Pro Pro Pro Pro Pro Gln Gln Leu Pro Lys Ala Ala					
	340		345		350
Ala Ala Ala Ala Pro Thr Gly Thr Glu Leu Lys Pro Ala Thr Ala Pro					
	355		360		365
Pro His Gly Ser Pro Arg Ala Asn Ser His Thr Val Thr Val Thr Pro					
	370		375		380
Pro Asn Val Pro Arg Ala Ala Ala Ala Thr Val Pro Thr Ala Gly Ala					

385		390		395		400									
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				405					410					415	
Pro	Val	Pro	Lys	Ala	Ala	Pro	Val	Thr	Pro	Pro	Ser	Pro	Gln	Gln	Ala
			420					425					430		
Val	Pro	Arg	Ala	Ala	Thr	Ala	Ala	Ala	Ala	Pro	Val	Thr	Pro	Gln	Gln
		435					440					445			
Pro	Val	Thr	Lys	Ala	Ala	Thr	Thr	Thr	Asn	Ala	Thr	Pro	Pro	Pro	Gln
	450					455					460				
Pro	Ile	Pro	Lys	Ala	Ala	Thr	Thr	Thr	Thr	Ala	Thr	Pro	Val	Thr	Pro
465				470						475				480	
Gln	Gln	Pro	Ile	Pro	Lys	Ala	Gly	Thr	Asp	Ala	Ala	Pro	Pro	Pro	Ala
			485						490					495	
Val	Pro	Lys	Ala	Pro	Ser	Asp	Gly	Arg	Ala	Ala	Thr	Pro	Gly	Val	Pro
		500						505					510		
Asn	Ala	Ala	Thr	Asp	Pro	Gln	Lys	Pro	Pro	Pro	Thr	Pro	Gln	Ser	Val
	515						520					525			
Pro	Ser	Ala	Val	Thr	Glu	Pro	Lys	Pro	Gln	Pro	Arg	Ala	Ala	Pro	Pro
	530					535					540				
Pro	Ser	Asn	Glu	Ala	Thr	Pro	Ala	Val	Pro	Ser	Pro	Ser	Pro	Asn	Leu
545				550					555					560	
Lys	Ser	Pro	Leu	Pro	Thr	Ile	Pro	Lys	Pro	Val	Pro	Leu	Met	Ala	Leu
			565					570					575		
Thr	Pro	Gln	Pro	Val	Thr	Ala	Gln	Met	Val	Thr	Gln	Leu	Ala	Ala	Thr
		580						585				590			
Lys	Pro	Ser	Pro	Ile	Val	Pro	Lys	Ala	Ser	Pro	Lys	Ala	Leu	Met	Thr
	595					600					605				
Pro	Pro	Pro	Pro	Pro	Pro	Gly	Leu	Pro	Arg	Ala	Leu	Ala	Ala	Ala	Lys
	610					615					620				
Leu	Leu	Gly	Leu	Pro	Ser	Ser	Pro	Val	Ala	Ser	Ala	Met	His	Ala	Lys
625				630						635				640	
Val	Thr	Pro	Arg	Pro	Leu	Pro	Ala	Ser	Pro	Val	Pro	Met	Ala	Ala	Ser

645	650	655
Pro Ala Ser Leu Gly Pro Asp Ala Ala Arg Val Ala Leu Ala Thr Asn		
660	665	670
Ala Ala Ser Pro Gly Ala Lys Pro Glu Ala Ala Gly Gly Asn Gly Thr		
675	680	685
Leu Met Ala Pro Met Gly Ala Ala Asn Thr Gln Met Ala Pro Ile Gly		
690	695	700
Ala Ala Gly Ala Ala Gln Thr Ala Pro Met Gly Ala Ala His Thr His		
705	710	715 720
Val Ser Pro Met Gly Ala Gly Gly Ala Thr Gln Met Ser Pro Thr Gly		
725	730	735
Ala Ala Asn Thr His Met Ser Pro Ile Gly Ala Gly Gly Ala Thr Gln		
740	745	750
Met Ser Pro Met Gly Ala Ala Asn Thr Gln Met Ser Pro Met Gly Ala		
755	760	765
Thr Thr Thr Gln Met Ser Pro Met Gly Ala Ala Ala Thr Thr Gln Pro		
770	775	780
Ser Pro Met Gly Ala Ala Ala Thr Gln Val Thr Ala Thr Ser Ala Gly		
785	790	795 800
Asn Thr Met Gln Val Ser Pro Met Gly Ala Ala Thr Pro Pro Gln Thr		
805	810	815
Pro Ser Val Gly Ala Ala Thr Thr Pro Gln Pro Ser Pro Met Gly Ala		
820	825	830
Ala Thr Thr Leu Met Ser Pro Met Gly Ala Ala Thr Thr Pro Gln Pro		
835	840	845
Ser Pro Met Gly Ala Val Thr Thr Gln Pro Pro Pro Met Ala Ala Thr		
850	855	860
Asn Thr Thr Gln Pro Pro Pro Met Ala Ala Ser Thr Pro Gln Ser Thr		
865	870	875 880
Pro Met Gly Ala Ala Thr Thr Thr Gln Ser Pro Pro Met Gly Ala Thr		
885	890	895
Thr Thr Gln Ser Pro Pro Met Gly Ala Ser Thr Pro Gln Ala Pro Pro		

900	905	910
Thr Val Ala Gly Ser Pro	Thr Pro Pro Pro Pro	Ile Pro Pro Ser Pro
915	920	925
Thr Ala Gln Thr Ser Pro	Gln Pro Met Ser Lys	Ser Pro Pro Pro Asp
930	935	940
Pro Pro Lys Ala Pro Ser	Ala Ala Ala Gln Thr	Ser Pro Ala Ala His
945	950	955
Val Ala Asn Ala Ser Pro	Gly Val Thr Ala Val	Ser Pro Ala Pro Ile
965	970	975
Gly Val Thr Glu Ala Ser	Pro Ser Ala Asp Gly	Ala Arg Leu Ser Pro
980	985	990
Gly Pro Thr Ala Ala Thr	Asp Gly Pro Lys Ala	Ser Pro Ala Ala Thr
995	1000	1005
Ala Asp Val Thr Glu Ala	Ala Thr Asp Val Thr	Ala Ala Thr Ala
1010	1015	1020
Val Pro Ala Glu Ala Ala	Pro Thr Lys Ala Lys	Arg Ser Ser Ser Ser
1025	1030	1035
Ser Ser Ser Ser Ser Ser	Ser Ser Ser Ser Ser	Ser Ser Ser Ser Ser
1045	1050	1055
Ser Ser Ser Ser Asp Ser	Asp Ser Ser Ser Ser	Ser Ser Glu Ser Asn
1060	1065	1070
Pro Ala Ser Pro Ala Pro	Ala Val Gly Asp Gly	Gln Gln Gln Met Thr
1075	1080	1085
Pro Gly Ala Ala Gln Ser	Val Pro Pro Val Thr	Glu Ala Ala Val Gln
1090	1095	1100
Glu Ala Ala Ala Ala Ala	Ala Ala Ala Ala Gly	Ala Glu Arg Glu Gly
1105	1110	1115
Arg Pro Thr Arg Arg Lys	Lys Arg Thr Arg Ser	Ser Ser Ser Ser Ser
1125	1130	1135
Ser Ser Ser Ser Ser Ser	Ser Ser Ser Ser Ser	Ser Ser Ser Ser Ser
1140	1145	1150



<210> 80  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

<400> 80  
 Met Asn Cys Val Cys Arg Leu Val Leu Val Val Leu Ser Leu Trp Pro  
 1 5 10 15  
 Asp Thr Ala Val Ala Pro Gly Pro Pro Pro Gly Pro Pro Arg Val Ser  
 20 25 30  
 Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr Arg Ser  
 35 40 45  
 Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp Lys Phe  
 50 55 60  
 Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu Ala Met  
 65 70 75 80  
 Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu Thr Arg  
 85 90 95  
 Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp Leu Arg  
 100 105 110  
 Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu Gly Thr  
 115 120 125  
 Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu Leu Met  
 130 135 140  
 Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala Pro Pro  
 145 150 155 160  
 Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala His Ala  
 165 170 175  
 Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg Gly Leu  
 180 185 190  
 Leu Leu Leu Lys Thr Arg Leu  
 195

<210> 81  
 <211> 1029

<212> DNA  
 <213> Homo sapiens

<400> 81  
 tctgctttta ataagcttcc caatcagctc tcgagtgcaa agcgcctctcc ctccctcgcc 60  
 cagccttcgt cctcctggcc cgctcctctc atccctccca ttctccattt cccttcctgt 120  
 ccctccctgt cagggcgtaa ttgagtcaaa ggcaggatca ggttccccgc cttccagtc 180  
 aaaaatcccg ccaagagagc cccagagcag aggaaaatcc aaagtggaga gaggggaaga 240  
 aagagaccag tgagtcaccc gtccagaagg cggggagagc agcagcggcc caagcaggag 300  
 ctgcagcgag ccgggtacct ggactcagcg gtagcaacct cgccccttgc aacaaaggca 360  
 gactgagcgc cagagaggac gtttccaact caaaaatgca ggctcaacag taccagcagc 420  
 agcgtcgaaa atttgcagct gccttcttgg cattcatttt catactggca gctgtggata 480  
 ctgctgaagc aggggaagaaa gagaaaccag aaaaaaaagt gaagaagtct gactgtggag 540  
 aatggcagtg gagtgtgtgt gtgccacca gtggagactg tgggctgggc acacgggagg 600  
 gcactcggac tggagctgag tgcaagcaaa ccatgaagac ccagagatgt aagatcccc 660  
 gcaactggaa gaagcaattt ggcgcggagt gcaaatacca gttccaggcc tggggagaat 720  
 gtgacctgaa cacagccctg aagaccagaa ctggaagtct gaagcgagcc ctgcacaatg 780  
 ccgaatgcca gaagactgtc accatctcca agccctgtgg caaactgacc aagcccaaac 840  
 ctcaagcaga atctaagaag aagaaaaagg aaggcaagaa acaggagaag atgctggatt 900  
 aaaagatgtc acctgtggaa cataaaaagg acatcagcaa acaggatcag ttaactattg 960  
 catttatatg taccgtaggc tttgtattca aaaattatct atagctaagt acacaataag 1020  
 caaaaacaa 1029

<210> 82  
 <211> 216  
 <212> PRT  
 <213> Homo sapiens

<400> 82  
 Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
 1 5 10 15  
 Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
 20 25 30  
 His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45  
 Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
 50 55 60  
 Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80  
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys  
210 215

<210> 83

<211> 346

<212> PRT

<213> Rattus norvegicus

<400> 83

Met Glu Leu Ala Pro Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro  
1 5 10 15

Glu Pro Pro Ala Glu Pro Arg Pro Leu Phe Gly Ile Gly Val Glu Asn  
20 25 30

Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val Leu  
35 40 45

Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly Lys  
50 55 60

Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala Asp  
65 70 75 80

Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr Ala  
85 90 95

Leu	Pro	Thr	Trp	Val	Leu	Gly	Ala	Phe	Ile	Cys	Lys	Phe	Ile	His	Tyr	100	105	110	
Phe	Phe	Thr	Val	Ser	Met	Leu	Val	Ser	Ile	Phe	Thr	Leu	Ala	Ala	Met	115	120	125	
Ser	Val	Asp	Arg	Tyr	Val	Ala	Ile	Val	His	Ser	Arg	Arg	Ser	Ser	Ser	130	135	140	
Leu	Arg	Val	Ser	Arg	Asn	Ala	Leu	Leu	Gly	Val	Gly	Phe	Ile	Trp	Ala	145	150	155	160
Leu	Ser	Ile	Ala	Met	Ala	Ser	Pro	Val	Ala	Tyr	Tyr	Gln	Arg	Leu	Phe	165	170	175	
His	Arg	Asp	Ser	Asn	Gln	Thr	Phe	Cys	Trp	Glu	His	Trp	Pro	Asn	Gln	180	185	190	
Leu	His	Lys	Lys	Ala	Tyr	Val	Val	Cys	Thr	Phe	Val	Phe	Gly	Tyr	Leu	195	200	205	
Leu	Pro	Leu	Leu	Leu	Ile	Cys	Phe	Cys	Tyr	Ala	Lys	Val	Leu	Asn	His	210	215	220	
Leu	His	Lys	Lys	Leu	Lys	Asn	Met	Ser	Lys	Lys	Ser	Glu	Ala	Ser	Lys	225	230	235	240
Lys	Lys	Thr	Ala	Gln	Thr	Val	Leu	Val	Val	Val	Val	Val	Phe	Gly	Ile	245	250	255	
Ser	Trp	Leu	Pro	His	His	Val	Ile	His	Leu	Trp	Ala	Glu	Phe	Gly	Ala	260	265	270	
Phe	Pro	Leu	Thr	Pro	Ala	Ser	Phe	Phe	Phe	Arg	Ile	Thr	Ala	His	Cys	275	280	285	
Leu	Ala	Tyr	Ser	Asn	Ser	Ser	Val	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Leu	290	295	300	
Ser	Glu	Asn	Phe	Arg	Lys	Ala	Tyr	Lys	Gln	Val	Phe	Lys	Cys	Arg	Val	305	310	315	320
Cys	Asn	Glu	Ser	Pro	His	Gly	Asp	Ala	Lys	Glu	Lys	Asn	Arg	Ile	Asp	325	330	335	
Thr	Pro	Pro	Ser	Thr	Asn	Cys	Thr	His	Val							340	345		

<210> 84  
 <211> 1308  
 <212> DNA  
 <213> Bos taurus

<400> 84  
 cgagcgcccg cagagctggg ctccgccaag ggaatgcgaa cgcgcaagga aggaaggatg 60  
 ccgcgggcgc cgagagagaa tgccacggcc cgggagcccc tggatcgcca ggagcccccg 120  
 ccgagggcgc agaggagacc ccagcgggcg ccgccacagc agcctgaagc tcgggagcct 180  
 cccggcaggg gcccgcgctt ggtgccccac gactacatgc tgtcaatcta caggacttac 240  
 tccatcgccg agaagctggg catcaatgct agctttttcc agtcttccaa gtcgggtaat 300  
 acgatcacta gctttgtaga caggggacta gacgatctct cgcacactcc tctccggaga 360  
 cagaagtatt tgtttgatgt gtccacgctc tcagacaaag aagagctggt gggcgcgagc 420  
 gtgcggtgtgt ttccgacggc gcccgctgcc ctggcgccgc cggcgggcgc tccgcttgca 480  
 gctcttcgcc tgccagtcgc cctgctgct ggaagcgcg agcctggacc cgcaggggag 540  
 ccccgggccc gctgggaagt cttegacgtg tggcgggggc tgcgccccca gccctggaag 600  
 cagctgtgct tggagcttcg ggccgctggt ggcggcgagc cggcgcgccgc ggaggacgag 660  
 gcgcgcacgc ctgggccccca gcagccgccc ccccgggacc tgcggagtct gggcttcggc 720  
 cggaggggtgc ggacccccca ggagcgcgcc ttgctcgtcg tgttctccag gtcccagcgc 780  
 aagaccctgt tcgcccagat gcgcgagcag ctgggctcgg cgaccgaggt ggtcggcccc 840  
 ggtggtgggg ccgagggggtc ggggcccgcg ccgcccgcgc cgcgcgcgc gccgtcgggc 900  
 acccgggacg ctgggctctg gtcgcccctc cctggccggc ggcggcgac ggccttcgcc 960  
 agccgccacg gcaagcggca cggcaagaag tcgaggtgct gctgcagcaa gaagcccctg 1020  
 cacgtgaact tcaaggagct gggctgggac gactggatta tcgcgcccct ggagtacgag 1080  
 gcctaccact gcgagggcgt gtgcgacttc ccgtacgct cgcacctgga gccaccaaac 1140  
 cacgccatca tccagacgct gatgaactcc atggaccccg gctccacccc gccagctgct 1200  
 tgcgtgccc ccaaatgac tccatcagc atcttgtaga tcgacgggg caataatgtg 1260  
 gtctacaacg agtacgagga gatggtggtg gactcgtgct gctgcagg 1308

<210> 85  
 <211> 436  
 <212> PRT  
 <213> Bos taurus

<400> 85  
 Arg Ala Ser Ala Glu Leu Gly Ser Ala Lys Gly Met Arg Thr Arg Lys  
 1 5 10 15  
 Glu Gly Arg Met Pro Arg Ala Pro Arg Glu Asn Ala Thr Ala Arg Glu  
 20 25 30  
 Pro Leu Asp Arg Gln Glu Pro Pro Pro Arg Pro Gln Glu Glu Pro Gln  
 35 40 45  
 Arg Arg Pro Pro Gln Gln Pro Glu Ala Arg Glu Pro Pro Gly Arg Gly

50		55		60
Pro Arg Leu Val	Pro His Glu Tyr Met Leu Ser Ile Tyr Arg Thr Tyr			
65	70	75	80	
Ser Ile Ala Glu Lys Leu Gly Ile Asn Ala Ser Phe Phe Gln Ser Ser				
	85	90	95	
Lys Ser Ala Asn Thr Ile Thr Ser Phe Val Asp Arg Gly Leu Asp Asp				
	100	105	110	
Leu Ser His Thr Pro Leu Arg Arg Gln Lys Tyr Leu Phe Asp Val Ser				
	115	120	125	
Thr Leu Ser Asp Lys Glu Glu Leu Val Gly Ala Asp Val Arg Leu Phe				
	130	135	140	
Arg Gln Ala Pro Ala Ala Leu Ala Pro Pro Ala Ala Ala Pro Leu Ala				
145	150	155	160	
Ala Leu Arg Leu Pro Val Ala Pro Ala Ala Gly Ser Ala Glu Pro Gly				
	165	170	175	
Pro Ala Gly Ala Pro Arg Pro Gly Trp Glu Val Phe Asp Val Trp Arg				
	180	185	190	
Gly Leu Arg Pro Gln Pro Trp Lys Gln Leu Cys Leu Glu Leu Arg Ala				
	195	200	205	
Ala Trp Gly Gly Glu Pro Gly Ala Ala Glu Asp Glu Ala Arg Thr Pro				
	210	215	220	
Gly Pro Gln Gln Pro Pro Pro Pro Asp Leu Arg Ser Leu Gly Phe Gly				
225	230	235	240	
Arg Arg Val Arg Thr Pro Gln Glu Arg Ala Leu Leu Val Val Phe Ser				
	245	250	255	
Arg Ser Gln Arg Lys Thr Leu Phe Ala Glu Met Arg Glu Gln Leu Gly				
	260	265	270	
Ser Ala Thr Glu Val Val Gly Pro Gly Gly Gly Ala Glu Gly Ser Gly				
	275	280	285	
Pro Pro Pro Pro Pro Pro Pro Pro Pro Ser Gly Thr Pro Asp Ala				
	290	295	300	
Gly Leu Trp Ser Pro Ser Pro Gly Arg Arg Arg Thr Ala Phe Ala				

305		310		315		320
Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg Leu Arg Cys Ser						
	325		330		335	
Lys Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp Asp Asp Trp						
	340		345		350	
Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly Val Cys						
	355		360		365	
Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Ile Ile						
	370		375		380	
Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro Pro Ser Cys						
	385		390		395	400
Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr Ile Asp Ala						
	405		410		415	
Gly Asn Asn Val Val Tyr Asn Glu Tyr Glu Glu Met Val Val Glu Ser						
	420		425		430	
Cys Gly Cys Arg						
	435					